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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 13:21:49 ; Search time 1037 Seconds
(without alignments)
5107.725 Million cell updates/sec

Title: US-09-762-105a-14

Perfect score: 182

Sequence: 1 gagctcgtccccgcgcgc.....tgactgtggacagcgtagc 182

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sv.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pin.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	182	100.0	5270	12	AF176637	AF176637 plastid t
2	111.2	61.1	168	6	AX076661	AX076661 Sequence
3	85.8	47.1	127	6	AX137514	AX137514 Sequence
4	85.8	47.1	127	6	E51179	E51179 Method for
5	85.8	47.1	127	6	E51197	E51197 Process for
6	85.8	47.1	766	8	CHNTRN1	J01453 Tobacco chl
7	85.8	47.1	2113	8	CHNTRN1	V00165 Tobacco chl
8	85.8	47.1	3274	8	CPV18934	Y18934 N.plumagin
9	85.8	47.1	7829	8	CHNTRN1	Y18934 Solanum nig
10	85.8	47.1	155939	8	CHNTRN1	Z00044 Nicotiana t
11	85.8	47.1	155939	8	CHNTRN1	Z00044 Nicotiana t
12	85.8	47.1	156687	8	ABE316582	AJ316582 Atropa be
13	85.8	47.1	156687	8	ABE316582	AJ316582 Atropa be
14	85.4	46.9	184	6	AR145914	AR145914 Sequence
15	85.4	46.9	300	6	AR171710	AR171710 Sequence
16	85.4	46.9	300	6	AR171711	AR171711 Sequence
17	85.4	46.9	2962	12	XXU12809	U12809 Transform
18	85.4	46.9	3019	12	XXU12810	U12810 Transform
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20	85.4	46.9	3136	12	AF061065	AF061065 plastid t
21	85.4	46.9	4126	12	XXU12814	U12814 Transform
22	85.4	46.9	4126	12	XXU12815	U12815 Transform
23	85.4	46.9	4174	12	XXU12812	U12812 Transform
24	85.4	46.9	4174	12	XXU12813	U12813 Transform
25	85.4	46.9	4304	12	AY005806	AY005806 Transform
26	85.4	46.9	7454	12	CTR312391	AJ312391 Chloropla
27	85.4	46.9	7626	12	CTR312392	AJ312392 Chloropla
28	85.4	46.9	7626	12	CTR312393	AJ312393 Chloropla
29	84.8	46.6	159	12	M23201	M23201 Synthetic c
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31	84.8	46.6	2731	1	PET31F1P	X62498 E.coli plas
32	84.8	46.6	2829	12	CVPRSET5C	X54204 Cloning vec
33	84.8	46.6	2829	12	CVPRSET6C	X54208 Cloning vec
34	84.8	46.6	2830	12	CVPRSET5B	X54203 Cloning vec
35	84.8	46.6	2830	12	CVPRSET6B	X54207 Cloning vec
36	84.8	46.6	2831	12	CVPRSET5A	X54206 Cloning vec
37	84.8	46.6	2831	12	CVPRSET6A	X54209 Expression
38	84.8	46.6	2894	12	CVT7NDE	I15353 Sequence 1
39	84.8	46.6	3984	6	I15353	I15353 Sequence 1
40	84.8	46.6	3993	12	CVPGEMEX1	X65317 Cloning vec
41	84.8	46.6	3995	12	CVPGEMEX2	X65318 Cloning vec
42	84.8	46.6	5231	6	AX001273	AX001273 Sequence
43	84.8	46.6	5953	6	AX191649	AX191649 Sequence
44	84.8	46.6	39937	7	T7CG	V01146 Genome of b
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ALIGNMENTS

RESULT 1
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LOCUS Plastid transformation vector pMSK49 plastid targeting region.
DEFINITION AF176637
ACCESSION AF176637
VERSION AF176637.1 GI:7637848
KEYWORDS
SOURCE Plastid transformation vector pMSK49.
ORGANISM Plastid transformation vector pMSK49
REFERENCE 1 (bases 1 to 5270)
AUTHORS Khan,M.S. and Maliga,P.
TITLE Fluorescent antibiotic resistance marker for tracking plastid
transformation in higher plants
JOURNAL Nat. Biotechnol. 17 (9), 910-915 (1999)

99403345 MEDLINE
10471936 PUBMED
2 (bases 1 to 5270)
Khan,M.S. and Maliga,P.
AUTHORS
Direct Submission
TITLE
Submitted (09-AUG-1999) Waksman Institute, Rutgers University, 190
Frelinhuyesen Road, Piscataway, NJ 08854, USA
JOURNAL
FEATURES
source
1. .5270
Location/Qualifiers
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/db_xref="taxon:120083"
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1. .1884
/organism="Oryza sativa"
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/db_xref="taxon:4530"
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1885. .1910
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1911. .2099
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complement(1911. .2099)
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/note="aminoglycoside 3'-adenyltransferase fused at its
C-terminus via the 11-mer ELAVEGKLEVA with the soluble
modified form of the Aequorea victoria green fluorescent
protein with GenBank Accession Number U70495; N-terminal
segment is the T7 phage gene 10 N-terminus"
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HSVALGPAAEELDPVPQDLFEALNETITLWNSPPDAGDERNVVILSLRIWYSAY
TGKAPKDAADNMRLEPAQYQVILEARQAVLGQEDRLASRADOLEEFVHYVKG
ITVVKELAVEGKLEVAASKEELFTGVVPLILVELDGNVGHKFSVSEGEVDATY
GKULAFICTIGTLPVPMPLVTFPSYVQVCSRPDPMKRDHDFKASMPGEYVQRTY
ISFDDGNYKTRAEVFEQDLYNRELKIDPKEDGNILGHKLEYNHNHVIITAD
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complement(3689. .3712)
/gene="aadA11gfp-S3"
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complement(2864. .3646)
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/note="Region: aminoglycoside 3'-adenyltransferase"
complement(2831. .2863)
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complement(2114. .2830)
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misc_feature complement(3683. .3858)
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misc_feature 3859. .3879
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Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 3864 GAGTCGCTCCCGCCGCTGTTCAATGAGATGAGAGCTGCTGGATTGACGTC 3805
|||||
QY 61 AGGGGCGAGGATGCTATATTTCTGGAGGAGACACACGTTTCCACTAGAAATA 120
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DB 3804 AGGGGCGAGGATGCTATATTTCTGGAGGAGACACACGTTTCCACTAGAAATA 3745
|||||
QY 121 ATTTTGTAACTTTAAGAGGAGATATACATATGGCAAGCATGACTGGTGGACAGCTA 180
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DB 3744 ATTTTGTAACTTTAAGAGGAGATATACATATGGCAAGCATGACTGGTGGACAGCTA 3685.
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QY 181 GC 182
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DB 3684 GC 3683
RESULT 2
AX076661 AX076661 168 bp DNA linear PAT 06-FEB-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0104331.
ACCESSION AX076661
VERSION AX076661.1 GI:12711193
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 168)
AUTHORS Staub,J.M.
TITLE Enhanced expression of proteins using gfp
PATENT: WO 0104331-A 1 18-JAN-2001;
Caigene LLC (US)
FEATURES
Location/Qualifiers
source
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/db_xref="taxon:32644"
BASE COUNT 45 a 31 c 51 g 41 t
ORIGIN
Query Match 61.1%; Score 111.2; DB 6; Length 168;
Best Local Similarity 88.7%; Pred. No. 5.1e-25;
Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;
QY 7 GCTCCCGCCGCTGCTTCAATGAGATGAGAGCTGCTGGATTGACGTAGAGGGG 66
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DB 23 GCTCCCGCCGCTGCTTCAATGAGATGAGAGCTGCTGGATTGACGTAGAGGGG 82
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QY 67 CAGGGATGCTATATTTCTGGAGGAGACACACGTTTCCACTAGAAATAATTTTG 126
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DB 83 CAGGGATGCTATATTTCTGGAGGAGACACACGTTTCCACTAGAAATAATTTTG 138
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QY 127 TTTAACTTTAAGAGGAGATATACATATGG 156
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DB 139 TTTAACTTTAAGAGGAGATATACCATCG 168
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RESULT 3
AX137514 AX137514 127 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 16 from Patent EP1076095.
ACCESSION AX137514

VERSION AX137514.1 GI:14273708
KEYWORDS common tobacco.
SOURCE Nicotiana tabacum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 127)
AUTHORS Yamaguchi, I., Nakashita, H., Yoshioka, K. and Doi, Y.
TITLE Methods for transformation of plants, transformed plants and
processes for preparation of polyesters
JOURNAL Patent: EP 1076095-A 16 14-FEB-2001;
Riken (JP)
FEATURES
source Location/Qualifiers
1. .127
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BASE COUNT 28 a 24 c 45 g 30 t
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Best Local Similarity 97.8%; Pred. No. 7.8e-17;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 TCCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGATTGACGTGAGGG 64
Db 11 TTGCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGATTGACGTGAGGG 70
QY 65 GCGAGGATGGCTATATTTCTGGGAGGA 93
Db 71 GCGAGGATGGCTATATTTCTGGGAGGA 99
RESULT 4
LOCUS E51179 127 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for transforming plant and transformed plant.
ACCESSION E51179
VERSION E51179.1 GI:18629496
KEYWORDS JP 2001046073-A/16.
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 127)
AUTHORS Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE Method for transforming plant and transformed plant
JOURNAL Patent: JP 2001046073-A 16 20-FEB-2001;
RIKAGAKU KENKYUSHO, HIDEO NAKASHITA
COMMENT OS Nicotiana tabacum (tobacco)
PN JP 2001046073-A/16
PD 20-FEB-2001
PF 09-AUG-1999 JP 1999225832
PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
PC C12N15/00, C12N5/00, C12N9/02, C12N9/10, C12P7/62, PC
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Best Local Similarity 97.8%; Pred. No. 7.8e-17;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 65 GCGAGGATGGCTATATTTCTGGGAGGA 93
Db 71 GCGAGGATGGCTATATTTCTGGGAGGA 99
RESULT 5
LOCUS E51197 127 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing polyester.
ACCESSION E51197
VERSION E51197.1 GI:18629514
KEYWORDS JP 2001046074-A/16.
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 127)
AUTHORS Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE Process for producing polyester
JOURNAL Patent: JP 2001046074-A 16 20-FEB-2001;
RIKAGAKU KENKYUSHO
COMMENT OS Nicotiana tabacum (tobacco)
PN JP 2001046074-A/16
PD 20-FEB-2001
PF 09-AUG-1999 JP 1999225839
PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
PC C12N15/00, C12N5/00, C12N9/02, C12N9/10, C12P7/62, PC
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Best Local Similarity 97.8%; Pred. No. 7.8e-17;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 TCCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGATTGACGTGAGGG 64
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QY 65 GCGAGGATGGCTATATTTCTGGGAGGA 93
Db 71 GCGAGGATGGCTATATTTCTGGGAGGA 99
RESULT 6
LOCUS TORCPTGVR 766 bp DNA linear PLN 18-APR-1994
DEFINITION Tobacco (N. tabacum) Val-tRNA gene and 16S rRNA gene 5' end.
ACCESSION J01453
VERSION J01453.1 GI:343519
KEYWORDS 16S ribosomal RNA; ribosomal RNA; transfer RNA; transfer RNA-Val.
SOURCE Tobacco (N. tabacum, var. bright yellow 4) chloroplast DNA, clone
pTci.
ORGANISM Chloroplast Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 766)
AUTHORS Tohdoh, N., Shinozaki, K. and Sugliura, M.

QY 5 TCCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGATTGACGTGAGGG 64
Db 11 TTGCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGATTGACGTGAGGG 70
QY 65 GCGAGGATGGCTATATTTCTGGGAGGA 93
Db 71 GCGAGGATGGCTATATTTCTGGGAGGA 99
RESULT 5
LOCUS E51197 127 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing polyester.
ACCESSION E51197
VERSION E51197.1 GI:18629514
KEYWORDS JP 2001046074-A/16.
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 127)
AUTHORS Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE Process for producing polyester
JOURNAL Patent: JP 2001046074-A 16 20-FEB-2001;
RIKAGAKU KENKYUSHO
COMMENT OS Nicotiana tabacum (tobacco)
PN JP 2001046074-A/16
PD 20-FEB-2001
PF 09-AUG-1999 JP 1999225839
PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
PC C12N15/00, C12N5/00, C12N9/02, C12N9/10, C12P7/62, PC
CC
FH Key Location/Qualifiers
FT source 1. .127
/organism="Nicotiana tabacum (tobacco)".
FEATURES
source Location/Qualifiers
1. .127
/organism="Nicotiana tabacum"
/db_xref="taxon:4097"
BASE COUNT 28 a 24 c 45 g 30 t
ORIGIN
Query Match 47.1%; Score 85.8; DB 6; Length 127;
Best Local Similarity 97.8%; Pred. No. 7.8e-17;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 TCCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGATTGACGTGAGGG 64
Db 11 TTGCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGATTGACGTGAGGG 70
QY 65 GCGAGGATGGCTATATTTCTGGGAGGA 93
Db 71 GCGAGGATGGCTATATTTCTGGGAGGA 99
RESULT 6
LOCUS TORCPTGVR 766 bp DNA linear PLN 18-APR-1994
DEFINITION Tobacco (N. tabacum) Val-tRNA gene and 16S rRNA gene 5' end.
ACCESSION J01453
VERSION J01453.1 GI:343519
KEYWORDS 16S ribosomal RNA; ribosomal RNA; transfer RNA; transfer RNA-Val.
SOURCE Tobacco (N. tabacum, var. bright yellow 4) chloroplast DNA, clone
pTci.
ORGANISM Chloroplast Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 766)
AUTHORS Tohdoh, N., Shinozaki, K. and Sugliura, M.

Tue May 27 10:47:37 2003

Sequence of a putative promoter region for the rRNA genes of tobacco chloroplast DNA

Nucleic Acids Res. 9 (20), 5399-5406 (1981)

82059514

7029469

tRNA sequence contributed on tape April 1983 by M. Sprinzl & D.H. Gauss; from their entry 2063 in Nucleic Acids Res. 11, r55-r103 (1983). [1] proposes bases 302 or 308 as possible sites for transcription initiation, based on an in vitro assay with E.coli RNA polymerase.

FEATURES

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ORIGIN

BatEII site.

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Best Local Similarity 97.8%; Pred. No. 9.3e-17;

Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCGCTCCCGCCGCTTCATGAGATGATGAAGAGGCTCGTGGGATTGAGTGAGGG 64

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QY 65 GGCAGGATGGCTATATTTCTGGGAGGCA 93

DB 489 GGCAGGATGGCTATATTTCTGGGAGGCA 517

RESULT 7

CHNTRN1

LOCUS

DEFINITION

2113 bp DNA linear PLN 31-MAR-1992

Accession

V00165 J01453

VERSION

16S ribosomal RNA; transfer RNA; transfer RNA-Val.

KEYWORDS

common tobacco.

SOURCE

Chloroplast Nicotiana tabacum

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 628 to 2113)

Tohdo, N. and Sugiyama, M.

THE COMPLETE NUCLEOTIDE SEQUENCE OF 16S RIBOSOMAL RNA GENE FROM TOBACCO CHLOROPLASTS

Gene 17 (2), 213-218 (1982)

JOURNAL

MEDLINE

82211820

PUBMED

7044901

REFERENCE

2 (bases 1 to 766)

Tohdo, N., Shinozaki, K. and Sugiyama, M.

Sequence of a putative promoter region for the rRNA genes of tobacco chloroplast DNA

Nucleic Acids Res. 9 (20), 5399-5406 (1981)

JOURNAL

MEDLINE

82059514

PUBMED

7029469

FEATURES

source

1..2113

/organism="Nicotiana tabacum"

/organelle="plastid:chloroplast"

/db_xref="taxon:4097"

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BASE COUNT

530 a 473 c 649 g 461 t

ORIGIN

Query Match 47.1% Score 85.8; DB 8; Length 2113;

Best Local Similarity 97.8%; Pred. No. 1e-16;

Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCGCTCCCGCCGCTTCATGAGATGATGAAGAGGCTCGTGGGATTGAGTGAGGG 64

DB 429 TTGCTCCCGCCGCTTCATGAGATGATGAAGAGGCTCGTGGGATTGAGTGAGGG 488

QY 65 GGCAGGATGGCTATATTTCTGGGAGGCA 93

DB 489 GGCAGGATGGCTATATTTCTGGGAGGCA 517

RESULT 8

CHNTRN1

LOCUS

DEFINITION

3274 bp DNA linear PLN 04-JUN-1993

N. plumbaginifolia chloroplast 16S rDNA, trnV and trnI genes for 16S ribosomal RNA, transfer RNA-Val and transfer RNA-Ile (5'exon).

Accession

X70938.1 GI:14352

VERSION

16S ribosomal RNA; inverted repeat; ribosomal RNA; transfer RNA; transfer RNA-Ile-gau; transfer RNA-Val-gac; trnI gene; trnV gene.

KEYWORDS

curled-leaved tobacco.

SOURCE

Chloroplast Nicotiana plumbaginifolia

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 2059 to 2418)

O'Neill, C., Horvath, G.V., Horvath, E., Dix, P.J. and Medgyesy, P.

Chloroplast transformation in plants: polyethylene glycol (PEG) treatment of protoplasts is an alternative to biolistic delivery systems

Plant J. 3 (5), 729-738 (1993)

JOURNAL

MEDLINE

93386194

PUBMED

8397038

REFERENCE

2 (bases 1 to 3274)

Horvath, G.V.

Direct Submission

Submitted (16-FEB-1993) G.V. Horvath, Biological Research Centre, Institute of plant phys., Hungarian Academy of Science, PO Box 521, 6701 Szeged, HUNGARY

LOCATION/QUALIFIERS

1..3274

/organism="Nicotiana plumbaginifolia"

/organelle="plastid:chloroplast"

/strain="wild type"

/db_xref="taxon:4092"

/haplotype="dioid"

/tissue_type="leaf"

/dev_stage="mature plant"

927..998

/gene="trnV"

927..998

/gene="trnV"

/product="tRNA-Val"

/note="codon recognized: GAC"

/anticodon="(pos:9/2..974,aa:Val)

1226..2714

/gene="16S rDNA"

1226..2714

/gene="16S rDNA"

/product="16S ribosomal RNA"

3015..3051

/gene="trnI"

3015..3051

/gene="trnI"

/product="tRNA-Ile"

/note="5'exon"

825 a 713 c 949 g 787 t

BASE COUNT

825 a 713 c 949 g 787 t

ORIGIN

Query Match 47.1% Score 85.8; DB 8; Length 3274;

Best Local Similarity 97.8%; Pred.No. 1.le-16;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCTCTCCCGCCGCTGTTCAATCAGAAATGATAAGAGGCTCTGGGATTGACGTGAGG 64
|||||
Db 1028 TTGCTCCCGCCGCTGTTCAATCAGAAATGATAAGAGGCTCTGGGATTGACGTGAGG 1087
|||||

QY 65 GGCAGGATGGCTATATTTCTGGGAGGA 93
|||||

Db 1088 GGCAGGATGGCTATATTTCTGGGAGGA 1116
|||||

RESULT 9
CPY18934/c

LOCUS
DEFINITION Solanum nigrum chloroplast trnA-Ala, trnA-Ile, 16S rRNA, trnA-Val,
rps12, rps7, ndhB genes.

ACCESSION Y18934
VERSION Y18934.1 GI:4688654
KEYWORDS 16S ribosomal rRNA; 16S rRNA gene; NADH dehydrogenase subunit; ndhB
gene; ribosomal protein S12; ribosomal protein S7; rps12 gene; rps7
gene; transfer RNA-Ala; transfer RNA-Ile; transfer RNA-Val;
trnA-Ala gene; trnA-Ile gene; trnA-Val gene.
black nightshade.

SOURCE
ORGANISM Plastid Solanum nigrum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 7829)
Kavanagh,T.A., Thanh,N.D., Lao,N.T., McGrath,N., Peter,S.O.,
Horvath,E.M., Dix,P.J. and Medgyesy,P.
Homeologous plastid DNA transformation in tobacco is mediated by
multiple recombination events
Genetics 152 (3), 1111-1122 (1999)
99318845
10388829

REFERENCE
2 (bases 1 to 7829)
Kavanagh,T.A.
Direct Submission
Submitted (19-APR-1999) T.A. Kavanagh, University of Dublin,
Department of Genetics, Trinity College, Dublin 2, IRELAND

FEATURES
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1. .7829
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/organelle="plastid"
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3797. .3869
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3797. .3869
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/number=2
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/translation="MSRRGTAEKTKAKSDPIYNRLNMLVNLILKHCKKSLAYQIIV
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WLAASRRPGRNMFAKLUSSELVDNAKGSGDAIRKKEETHRAEANRAFAHR"
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BASE COUNT    2163 a   1916 c   1671 g   2079 t
ORIGIN

Query Match          47.1%; Score 85.8; DB 8; Length 7829;
Best Local Similarity 97.8%; Pred. No. 1.2e-16;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 TCGCCTCCCGCGCGTTCATATGAAGAAGGCTCGTGCGATTGACGTGAGGG 64
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Db      3768 TTGCTCCCGCGCGTTCATATGAGATGATGAAGAGCTCGTGCGATTGACGTGAGGG 3709
        |||||||

QY      65 GCAGGAGTGGCTATATTTCTGGGAGGA 93
        |||||||
Db      3708 GGCAGGAGTGGCTATATTTCTGGGAGCA 3680
        |||||||

RESULT 10
CHNTXX
LOCUS       Nicotiana tabacum chloroplast genome DNA.
DEFINITION Z00044.S54304
ACCESSION  Z00044.1 GI:2924257
VERSION    16S ribosomal RNA; 23S ribosomal RNA; 4.5S ribosomal RNA; 5S
KEYWORDS   ribosomal RNA; acetyl-CoA carboxylase; ATP synthase; ATP-dependent
           protease; autonomous replication; chloroplast; circular; complete
           genome; cytochrome b/f complex; cytochrome b6; cytochrome f;
           initiation factor; inverted repeat; maturase; NADH dehydrogenase;
           PSI 9kD protein; PSI I-protein; PSI J-protein; PSI P700 apoprotein;
           PSII 10kD phosphoprotein; PSII 32kD protein; PSII 44kD protein;
           PSII 47kD protein; PSII cytochrome b559; PSII D2 protein; PSII
           I-protein; PSII J-protein; PSII K-protein; PSII L-protein; PSII
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SOURCE ORGANISM	M-protein; PSII N-protein; PSII T-protein; replication origin; ribosomal protein L14; ribosomal protein L16; ribosomal protein L2; ribosomal protein L20; ribosomal protein L22; ribosomal protein L23; ribosomal protein L32; ribosomal protein L33; ribosomal protein L36; ribosomal protein S11; ribosomal protein S12; ribosomal protein S14; ribosomal protein S15; ribosomal protein S16; ribosomal protein S18; ribosomal protein S19; ribosomal protein S4; ribosomal protein S8; ribulose biphosphate carboxylase; RNA polymerase; small plastid RNA; unidentified reading frame.	JOURNAL COMMENT
	common tobacco.	
REFERENCE AUTHORS	Plakoyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliopsida; Solanales; Solanaceae; Nicotiana. Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.	Submitted (27-FEB-1998) T. Tsudzuki, Data Processing Center, Aichi-Gakuin University, 12 Arai-ke, Iwasaki, Nisshin, Aichi 470-0195, JAPAN On or before Jan 17, 2002 this sequence version replaced gi:264799, gi:11807. The circular tobacco chloroplast DNA sequence is presented in a linearized form by cutting at the junction (JLA) between IRA and LSC. JLA is designated zero and numbered proceeding towards LSC. The DNA strand which codes for the large subunit of ribulose 1,5-bisphosphate carboxylase is designated as A strand and the complementary strand as B strand. Nucleotide sequence of the B strand is presented. Large single copy region (LSC): repeat B (IRB): 112028 - 130598 (18571 bp) Inverted repeat A (IRA) region (SSC): 130599 - 155939 (25341 bp) An alphabetical index of tobacco chloroplast genes and ORFs GENE NUCLEOTIDE NUMBER (FROM)
	1 (bases 1 to 155844) Tanaka, M., Wakasugi, T., Hayashida, N., Shinzaki, K., Ohme, M., Zaita, N., Chunwongse, J., Obokata, B. Y., Sugita, M., Yamaguchi-Shinozaki, K., Ohto, C., Torazawa, K., Meng, J. F., Kato, A., Deno, H., Kamogashira, T., Yamada, K., Kusuda, J., Takaiwa, F., Tohdoh, N., Shimada, H., and Sugitara, M. The complete nucleotide sequence of tobacco chloroplast genome: its gene organization and expression EMBO J. 5, 2043-2049 (1986)	accD 59793 ars1 112862 ars2 14569 atpA 12148 atpB 56777 atpE 55284 atpF 13452 atpH 14099 atpI 16000 atpJ 74507 clpP 82495 infA 3658 matK 123933 ndhA 29261, 143365 ndhB 52667 ndhC 119025 ndhD 119935 ndhE 114292 ndhF 120709 ndhG 125116 ndhH 121609 ndhI 51465 ndhJ 52425 ndhK 48941 ORF70A 102102, 140524 ORF70B 46472 ORF74 110824, 131802 ORF75 96556, 146070 ORF79 96119, 146307 ORF92 66176 ORF99 67588 ORF103 37566 ORF105 96407, 146219 ORF115 102346, 140280 ORF131 111029 ORF350 104769, 137776 oriA 111778, 130606 oriB 64335 petA 77452 petB 79043 petD 68570 petG 68293 petL 43486 psaA 41208 psaB 119389 psaC 62083 psaI 69565 psaJ 1595 psaK 74953 psbA 35515 psbB 34470 psbD 67129 psbE 66868 psbF 77101 psbH 8398 psbI
TITLE	Shimada, H. and Sugitara, M. Fine structural features of the chloroplast genome: comparison of the sequenced chloroplast genomes Nucleic Acids Res. 19 (5), 983-995 (1991)	
	1 91212240 1708498	
JOURNAL MEDLINE PUBMED	Mitchelson, K. and Stephen, J. Processing of histidine transfer RNA precursors in tobacco chloroplasts Nucleic Acids Res. 19 (11), 3150 (1991)	
	91279477 2057370	
REFERENCE AUTHORS	4 (bases 31640 to 32290; 90230 to 91610) Aylliffe, M. A. and Timmis, J. N. Plastid DNA sequence homologies in the tobacco nuclear genome Mol. Gen. Genet. 236 (1), 105-112 (1992)	
	93156674 1337369	
JOURNAL MEDLINE PUBMED	5 (bases 1 to 155844) Morton, B. R. and Clegg, M. T. A chloroplast DNA mutational hotspot and gene conversion in a noncoding region near rbcL in the grass family (Poaceae) Curr. Genet. 24 (4), 357-365 (1993)	
	94073993 8252846	
REFERENCE AUTHORS	6 (bases 1 to 155939) Nadot, S., Bittar, G., Carter, L., Lacroix, R. and Lejeune, B. A phylogenetic analysis of monocotyledons based on the chloroplast gene rps4, using parsimony and a new numerical phenetics method Mol. Phylogenet. Evol. 4 (3), 257-282 (1995)	
	96111502 8845963	
JOURNAL MEDLINE PUBMED	7 (bases 1 to 155844) Kunimailayyan, M. and Nielsen, B. L. Fine mapping of replication origins (ori A and ori B) in Nicotiana tabacum chloroplast DNA Nucleic Acids Res. 25 (18), 3681-3686 (1997)	
	97426512 9278490	
REFERENCE AUTHORS	8 Sugitara, M. Direct Submission Submitted (12-AUG-1986)	
	9 (bases 1 to 155939) Tsudzuki, T. Direct Submission	

[illegible]

MGYLSVRINPSMVRQSENFIIINNAIKFDTLYPIIPLIGSLAKNEFTVLGHPI
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	Matches 87;	Conservative	0;	Mismatches 2;	Indels 0;
	Gaps				
Qy	5	TCGCTCCCGCCGCGCTTCAATGAGATGGATGAAGAGGCTCGTGGATTCGAGCTGAGG	64		
Db	102861	TTGCTCCCGCCGCGCTTCAATGAGATGAATGATGAGAGGCTCTGGGTTCGAGCTGAGG	102920		
Qy	65	GGCAGGGATGGCTATATTTCTTCGGGGGGA	93		
Db	102921	TTTTTGGGTATATATTTCTTGGGAGCA	102949		

RESULT 13	
ABE316582/c	
LOCUS	circular PLN 05-APR-2002
DEFINITION	DNA
ACCESSION	156687 bp
VERSION	Complete plasmid Chromosome, strain AB5p(kan).
KEYWORDS	
ABE316582	belladonna
AJ1316582	GI:20068310
AJ1316582	16S ribosomal RNA; 23S ribosomal RNA; 4.5S ribosomal RNA; 5S ribosomal RNA; accD gene; acetyl-CoA carboxylase beta subunit; ATP-dependent protease; atpA gene; ATPase alpha subunit; ATPase beta subunit; ATPase epsilon subunit; ATPase subunit I; ATPase subunit III; ATPase subunit IV; atpB gene; atpE gene; atpF gene; atpH gene; atpI gene; catalytic subunit; ccsA gene; ccsA protein; required for heme-attachment to c-type cytochromes; cemaA gene; clpp gene; Cyt b6/f complex subunit IV; cyt b6/f complex subunit VI; cytochrome b6/f complex subunit V; cytochrome b6; cytochrome b6/f complex subunit N; cytochrome f; matK gene; maturase; NADH dehydrogenase ND6 subunit; NADH dehydrogenase 18kD subunit; NADH dehydrogenase 19kD subunit; NADH dehydrogenase 32kD subunit; NADH dehydrogenase 49kD subunit; NADH dehydrogenase ND1 subunit; NADH dehydrogenase ND2 subunit; NADH dehydrogenase ND3 subunit; NADH dehydrogenase ND4 subunit; NADH dehydrogenase ND4L subunit; NADH dehydrogenase ND5 subunit; ndhA gene; ndhB gene; ndhC gene; ndhD gene; ndhE gene; ndhG gene; ndhH gene; ndhI gene; ndhJ gene; ndhK gene; ndhK gene; ORF 489; beta gene; petB gene; petD gene; petG gene;

gene; petL gene; petN gene; potential heme-binding protein; PSI
P700 apoprotein A1; psaA gene; psab gene; psac gene; psat gene;
psaj gene; psak gene; psbb gene; psbc gene; psbd gene; psbe
gene; psbf gene; psbg gene; psbi gene; psbj gene; psbk gene;
psbm gene; psbn gene; psbt gene; PSI 9KD protein; PSI
apoprotein A2; PSI reaction center subunit VII_L; PSI 10KD
phosphoprotein A2; PSI reaction center subunit VIII_L; PSI
protein; PSI D2 protein; PSI I protein; PSI K protein; PSI M
protein; PSI N protein; PSI II reaction center subunit IX; PSI
reaction center subunit V; PSI reaction center subunit VI; PSI
reaction center subunit X; PSI reaction center subunit XII; PSII
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L16; ribosomal protein L2; ribosomal protein L23; ribosomal protein
L22; ribosomal protein L3; ribosomal protein L32; ribosomal protein
L33; ribosomal protein L36; ribosomal protein S11; ribosomal
protein S12; ribosomal protein S13; ribosomal protein S18;
ribosomal protein S14; ribosomal protein S19; ribosomal protein
S19; ribosomal protein S2; ribosomal protein S3; ribosomal protein
S4; ribosomal protein S7; ribosomal protein S8; RNA polymerase
alpha subunit; RNA polymerase beta subunit; RNA polymerase beta'
subunit; RNA polymerase beta subunit; rpl14 gene; rpl16 gene;
rpl2 gene; rpl20 gene; rpl22 gene; rpl23 gene; rpl32 gene; rpl33
gene; rpl36 gene; rpoA gene; rpoB gene; rpoC1 gene; rpoC2 gene;
rps11 gene; rps12 gene; rps4 gene; rps5 gene; rps16 gene; rps18
gene; rps19 gene; rps2 gene; rps3 gene; rps4 gene; rps7 gene; rps8
gene; rnl6 gene; rnf23 gene; rnf45 gene; rnf5 gene; rubisco large
subunit; transfer RNA-Ala (GUC); transfer RNA-Arg (ACG); transfer
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transfer RNA-Cys (GCA); transfer RNA-fm (CAU); transfer RNA-Gln
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tRNA-His (GUG) gene; tRNA-Leu (UAA) gene; tRNA-Leu (UAG) gene;
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protein; ycf9 gene; ycf9 protein.

protein; four genes, for example, in belladonna

Atropa belladonna
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Atropa.

1 Schmitz-Linneweber, C., Reegl, R., Gia Du, T., Hupfer, H.,
Herrmann, R.G. and Maier, R., 1997. The nucleotide sequence of the plastid chromosome of *Atropa belladonna* (deadly nightshade) and its comparison with that of *Nicotiana tabacum* with emphasis on sequence elements relevant for microevolution

Unpublished
2 (bases 1 to 156687)
Schmitz-Linneweber, C.
Direct Submission
Submitted (24-MAY-2000) Schmitz-Linneweber C., Botanisches
Institut, Ludwig Maximilians Universität München, Menzinger Str.
67, München, Bavaria 80638, Germany

Location/Qualifiers
1. .156687
/organism="Atropa belladonna"
/strain="Ab5p(kan)"

FEATURES
source

Q*	complement(4324..4360) /gene="trna-Lys (UUU)" /product="trna-Lys" /note="codon recognized: AAA" complement(4324..4360) /gene="trna-Lys (UUU)" /number=1 complement(5050..6138) /gene="rps16" complement(join(5050..5276,6099..6138)) /gene="rps16" /codon_start=1 /product="ribosomal protein S16" /protein_id="CAC88026.1" /db_xref="GI:20068313" /translation="MWKRLRKRGKQRAVYRIVADVRSRRGKDLRKVGFDYDPIKN QTVLNPAFLYFEKGAAQPTGTVDILKKAENVKELRPNPKN"
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gene	
CDS	
intron	
exon	
gene	
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Query Match	47.1%; Score 85.8; DB 8; Length 156687;
Best Local Similarity	97.8%; Pred. No. 1.1e-16;
Matches	87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy	65 GGCAGGAGTGCTATATTTCTGGGAGGGA 93
Db 140636	GGCAGGAGTGCTATATTTCTGGGAGGGA 140608
RESULT 14	
ARI145914	
LOCUS	ARI145914 184 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 3 from patent US 6218145.
ACCESSION	ARI145914
VERSION	ARI145914.1 GI:15109103
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 184)
AUTHORS	Bogorian,G., O'Neill,J.P. and Staub,J.M.
TITLE	Bacterial expression systems based on plasmic or mitochondrial promoter combinations
JOURNAL	Patent: US 6218145-A 3 17-APR-2001;
FEATURES	Location/Qualifiers 1..184 /organism="unknown"
BASE COUNT	49 a 33 c 59 g 43 t
ORIGIN	
Query Match	46.9%; Score 85.4; DB 6; Length 184;
Best Local Similarity	98.9%; Pred. No. 1.1e-16;
Matches	86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	7 GCTCCCGCCGCTGTTCAATGAGATGATGAGAGGCTCGTGGGATTGACGTGAGGGG 66

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Db      2  GCTCCCCCGCGCTGTCATGAGATGGATAGAGCGCTCGTGGGATTGACGTGAGGGGG 61
QY      67  CAGGGATGGCTATATTTCTGGGAGCGA 93
Db      62  CAGGGATGGCTATATTTCTGGGAGCGA 89

RESULT 15
ARI71710      300 bp      DNA      linear      PAT 17-DEC-2001
LOCUS      ARI71710
DEFINITION      Sequence 4 from patent US 6297054.
ACCESSION      ARI71710
VERSION      ARI71710.1  GI:17910660
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 300)
AUTHORS      Maliga, P., Carrer, H. and Chaudhuri, S.
TITLE      Editing-based selectable plastid marker genes
JOURNAL      Patent: US 6297054-A 4 02-OCT-2001;
FEATURES
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BASE COUNT      90 a      63 c      86 g      61 t
ORIGIN

Query Match      46.9%; Score 85.4; DB 6; Length 300;
Best Local Similarity 98.9%; Pred. NO. 1.1e-16;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      7  GCTCCCCCGCGCTGTCATGAGATGGATAGAGCGCTCGTGGGATTGACGTGAGGGGG 66
Db      17  GCTCCCCCGCGCTGTCATGAGATGGATAGAGCGCTCGTGGGATTGACGTGAGGGGG 76
QY      67  CAGGGATGGCTATATTTCTGGGAGCGA 93
Db      77  CAGGGATGGCTATATTTCTGGGAGCGA 103

Search completed: May 25, 2003, 14:05:05
Job time : 1177 secs
```

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 13:38:09 ; Search time 61 Seconds
(without alignments)
915,003 Million cell updates/sec

Title: US-09-762-105A-14
Perfect score: 182
Sequence: 1 gagctcgctccccccgctc.....tgactgggtggacagggctagc 182

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA: *
1: /cgn2.6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2.6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2.6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2.6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2.6/ptodata/2/ina/PCTUS_COMB.seq: *
6: /cgn2.6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89.6	49.2	171	1	US-08-217-360-16
2	86.4	47.5	129	2	US-08-189-256A-25
3	86.4	47.5	129	4	US-09-193-853-25
4	86	47.3	140	2	US-08-189-256A-19
5	86	47.3	164	2	US-08-189-256A-26
6	86	47.3	164	4	US-09-193-853-26
7	86	47.3	164	2	US-08-189-256A-18
8	85.4	46.9	161	2	US-09-193-853-18
9	85.4	46.9	165	2	US-08-189-256A-4
10	85.4	46.9	165	4	US-09-193-853-4
11	85.4	46.9	168	2	US-08-189-256A-2
12	85.4	46.9	168	4	US-09-193-853-2
13	85.4	46.9	168	4	US-09-283-419-3
14	85.4	46.9	168	4	US-08-189-256A-24
15	85.4	46.9	258	2	US-08-189-256A-24
16	85.4	46.9	258	4	US-09-193-853-24
17	85.4	46.9	300	4	US-09-202-316-4
18	85.4	46.9	300	4	US-09-202-316-7
19	85.4	46.9	1134	2	US-08-189-256A-10
20	85.4	46.9	1134	4	US-09-193-853-10
21	85.4	46.9	1143	4	US-09-142-114B-6
22	85.4	46.9	1208	2	US-08-189-256A-28
23	85.4	46.9	1208	4	US-09-193-853-28
24	85.4	46.9	1416	2	US-08-189-256A-27
25	85.4	46.9	1416	4	US-09-193-853-27
26	85.4	46.9	1417	4	US-09-142-114B-7
27	85.4	46.9	1417	4	US-08-189-256A-3
C 27	85.4	46.9	2962	2	US-08-189-256A-3

C 28	85.4	46.9	2962	4	US-09-193-853-3	Sequence 3, Appl
29	84.8	46.6	3984	1	US-08-040-753-1	Sequence 1, Appl
30	83.8	46.0	105	4	US-09-597-877-9	Sequence 9, Appl
31	83.2	45.7	187	1	US-08-096-182A-7	Sequence 7, Appl
32	83.2	45.7	187	1	US-08-877-109-7	Sequence 7, Appl
33	83.2	45.7	187	3	US-08-798-760-7	Sequence 7, Appl
34	83.2	45.7	187	5	PCR-US94-08327-7	Sequence 7, Appl
35	83	45.6	139	1	US-08-217-360-13	Sequence 13, Appl
36	83	45.6	146	1	US-08-217-360-17	Sequence 17, Appl
37	82.8	45.5	104	2	US-08-722-806A-9	Sequence 9, Appl
38	82.8	45.5	104	4	US-09-337-028-9	Sequence 9, Appl
39	82.2	45.2	150	2	US-08-189-256A-1	Sequence 1, Appl
40	82.2	45.2	150	4	US-09-193-853-1	Sequence 1, Appl
41	72.2	39.7	146	2	US-08-302-623-44	Sequence 44, Appl
42	71	39.0	4411	2	US-08-929-967-5	Sequence 5, Appl
C 42	71	39.0	5443	2	US-08-929-967-1	Sequence 1, Appl
44	71	39.0	5616	2	US-08-929-967-3	Sequence 3, Appl
45	70.8	38.9	369	4	US-09-265-919-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-217-360-16
; Sequence 16, Application US/08217360
; Patent No. 5530191
; GENERAL INFORMATION:
; APPLICANT: MALIGA, Pal
; TITLE OF INVENTION: METHODS FOR PRODUCING CYTOPLASMIC
; TITLE OF INVENTION: MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF H
; TITLE OF INVENTION: SEED
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESS: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,360
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers University
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)563-4100
; TELEFAX: (215)563-4044
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-217-360-16

Query Match 49.2%; Score 89.6; DB 1; Length 171;
Best Local Similarity 78.3%; Pred. No. 1.4e-21;
Matches 130; Conservative 0; Mismatches 14; Indels 22; Gaps 1;
QY 7 GCTCCCCCGCGTCTTCATGAGATGAGGCTCGTGGGATGACGTGAGGGGG 66

Db 6 GCTCCCCCGCGCTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 65

QY 67 CAGGATGGCTATATTTCTGGGAGGAGACCAACGCTTTCC 110

Db 66 CAGGATGGCTATATTTCTGGGAGGAGAACTCCGGGCGAATTCAC 109

RESULT 3

US-09-193-853-25

Sequence 25, Application US/09193853

Patent No. 6388168

GENERAL INFORMATION:

APPLICANT: Maliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carrier, Helaine

APPLICANT: Kanevski, Ivan

TITLE OF INVENTION: DNA Constructs and Methods for Stably

TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and

TITLE OF INVENTION: Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09193,853

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA: US 07/518,763

APPLICATION NUMBER: 08/189,256

FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-193-853-25

Query Match 47.5%; Score 86.4; DB 4; Length 129;

Best Local Similarity 89.4%; Pred. No. 1.5e-20;

Mismatches 11; Indels 0; Gaps 0;

Matches 93; Conservative

QY 7 GCTCCCCCGCGCTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 66

Db 6 GCTCCCCCGCGCTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 65

QY 67 CAGGATGGCTATATTTCTGGGAGGAGCAACGCTTTCC 110

Db 66 CAGGATGGCTATATTTCTGGGAGGAGAACTCCGGGCGAATTCAC 109

Db 1 GCTCCCCCGCGCTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 60

QY 67 CAGGATGGCTATATTTCTGGGAGGAGCAACG 104

Db 61 CAGGATGGCTATATTTCTGGGAGGAGCAATTTGGAGCGAATTCGCGGGA 120

QY 105 TTTCCCACTAGAAATAATTTCTTAACTTAAGAGGAGATATAC 150

Db 121 ATTAGATCTAGAAATAATTTCTTAACTTAAGAGGAGATATAC 166

RESULT 2

US-08-189-256A-25

Sequence 25, Application US/08189256A

Patent No. 5877402

GENERAL INFORMATION:

APPLICANT: Maliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carrier, Helaine

APPLICANT: Kanevski, Ivan

TITLE OF INVENTION: DNA Constructs and Methods for Stably

TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and

TITLE OF INVENTION: Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08189,256A

FILING DATE: 31-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA: US 08/111,398

APPLICATION NUMBER: 25-AUG-1993

FILING DATE: 25-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-189-256A-25

Query Match 47.5%; Score 86.4; DB 2; Length 129;

Best Local Similarity 89.4%; Pred. No. 1.5e-20;

Mismatches 11; Indels 0; Gaps 0;

Matches 93; Conservative

QY 7 GCTCCCCCGCGCTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 66

RESULT 4
US-08-189-256A-19
; Sequence 19, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-189-256A-19

Query Match 47.3%; Score 86; DB 2; Length 140;
Best Local Similarity 90.2%; Pred. No. 2.le-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 7 GCTCCCGCGCGTTCATGAGTAAGAGGCTCGTGGGATGACGTGAGGGG 66
Db 17 GCTCCCGCGCGTTCATGAGTAAGAGGCTCGTGGGATGACGTGAGGGG 76
Qy 67 CAGGGATGGCTATATTTCTGGGAGGAGACCAACACGGTTTC 108
Db 77 CAGGGATGGCTATATTTCTGGGAGGCGAACTCCGGGCGAATTC 118

RESULT 5
US-09-193-853-19
; Sequence 19, Application US/09193853

Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/193,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-193-853-19

Query Match 47.3%; Score 86; DB 4; Length 140;
Best Local Similarity 90.2%; Pred. No. 2.le-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 7 GCTCCCGCGCGTTCATGAGTAAGAGGCTCGTGGGATGACGTGAGGGG 66
Db 17 GCTCCCGCGCGTTCATGAGTAAGAGGCTCGTGGGATGACGTGAGGGG 76
Qy 67 CAGGGATGGCTATATTTCTGGGAGGAGACCAACACGGTTTC 108
Db 77 CAGGGATGGCTATATTTCTGGGAGGCGAATTC 118

RESULT 6
US-08-189-256A-26
; Sequence 26, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
US-09-193-853-26

Query Match 47.3%; Score 86; DB 4; Length 164;
Best Local Similarity 90.2%; Pred. No. 2.3e-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 66

QY 7 GTCCTCCCGCGCTGTCATGAGATGGATAAGAGCGCTCGTGGGATTGACGTGAGGGG 66
DB 6 GTCTCCCGCGCTGTCATGAGATGGATAAGAGCGCTCGTGGGATTGACGTGAGGGG 66
QY 67 CAGGGATGCGTATATTTCTGGGGGAGACACACCGTTTC 108
DB 66 CAGGGATGCGTATATTTCTGGGGAGCACTCCGGCGCAATTC 107

RESULT 8
US-08-189-256A-18
Sequence 18, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
Transforming Plastids of Multicellular Plants
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman

APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Carreel, Helaine
 APPLICANT: Kanevski, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably
 TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
 TITLE OF INVENTION: Expressing Recombinant Proteins Therein
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dann, Dorffman, Herrell and Skillman
 STREET: 1601 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/189,256A
 APPLICATION NUMBER: US/08/189,256A
 FILING DATE: 31-JAN-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/111,398
 FILING DATE: 25-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 164 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-189-256A-26

Query Match 47.3%; Score 86; DB 2; Length 164;
 Best Local Similarity 90.2%; Pred. No. 2.3e-20;
 Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCTCGTTCAATGAGTAAGGCTCGTGGATTGACGTGAGGGG 66
 DB 6 GCTCCCGCCGCTCGTTCAATGAGTAAGGCTCGTGGATTGACGTGAGGGG 65
 QY 67 CAGGGATGCTATATTCTGGGGGAGACCAACACGGTTTC 108
 DB 66 CAGGGATGCTATATTCTGGGGGAGCACTCCGGGCGAATTC 107

RESULT 7
 US-09-193-853-26
 ; Sequence 26 Application US/09193853
 ; Patent No 6386168
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliga, Pal
 ; APPLICANT: Svab, Zora
 ; APPLICANT: Staub, Jeffrey
 ; APPLICANT: Zoubenko, Oleg V.
 ; APPLICANT: Allison, Lori A.
 ; APPLICANT: Carreel, Helaine
 ; APPLICANT: Kanevski, Ivan

STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-18

Query Match 46.9%; Score 85.4; DB 2; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCGCGTTCATGAGATGAGTAAAGAGGCTCGTGGATTGACGTGAGGGG 66
|||||
Db 23 GCTCCCGCGCGTTCATGAGATGAGTAAAGAGGCTCGTGGATTGACGTGAGGGG 82
|||||

QY 67 CAGGATGGCTATATTTCTGGAGGGA 93
|||||
Db 83 CAGGATGGCTATATTTCTGGAGGGA 109
|||||

RESULT 9
US-09-193-853-18
Sequence 18, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-18

Query Match 46.9%; Score 85.4; DB 4; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCGCGTTCATGAGATGAGTAAAGAGGCTCGTGGATTGACGTGAGGGG 66
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Db 23 GCTCCCGCGCGTTCATGAGATGAGTAAAGAGGCTCGTGGATTGACGTGAGGGG 82
|||||

QY 67 CAGGATGGCTATATTTCTGGAGGGA 93
|||||
Db 83 CAGGATGGCTATATTTCTGGAGGGA 109
|||||

RESULT 10
US-08-189-256A-4
Sequence 4, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

Tue May 27 10:47:40 2003

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/111,398
APPLICATION NUMBER: 36,252
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA: US 07/518,763
APPLICATION NUMBER: 36,252
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-4

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Query Match 45.9%; Score 85.4; DB 2; Length 165;
Best Local Similarity 98.9%; Pred. No. 3.7e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCCCGCTTCATGAGTGAAGAGGCTCGTGGATTGACGTGAGGGG 66
DB 1 GCTCCCCCGCTTCATGAGTGAAGAGGCTCGTGGATTGACGTGAGGGG 60

QY 67 CAGGATGGCTATATTCCTGGAGGGA 93
DB 61 CAGGATGGCTATATTCCTGGAGGGA 87

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RESULT 11
US-09-193-853-4
Sequence 4, Application US/09/193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TRANSFORMING PLASTIDS OF MULTICELLULAR PLANTS AND
EXPRESSING RECOMBINANT PROTEINS THEREIN
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

```

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APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-4

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Query Match 45.9%; Score 85.4; DB 4; Length 165;
Best Local Similarity 98.9%; Pred. No. 3.7e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCCCGCTTCATGAGTGAAGAGGCTCGTGGATTGACGTGAGGGG 66
DB 1 GCTCCCCCGCTTCATGAGTGAAGAGGCTCGTGGATTGACGTGAGGGG 60

QY 67 CAGGATGGCTATATTCCTGGAGGGA 93
DB 61 CAGGATGGCTATATTCCTGGAGGGA 87

```

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RESULT 12
US-08-189-256A-2
Sequence 2, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TRANSFORMING PLASTIDS OF MULTICELLULAR PLANTS AND
EXPRESSING RECOMBINANT PROTEINS THEREIN
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/111,398
APPLICATION NUMBER: 36,252
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA: US 07/518,763
APPLICATION NUMBER: 36,252
FILING DATE: 01-MAY-1990

```

ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-2

Query Match 46.9%; Score 85.4; DB 2; Length 168;
Best Local Similarity 98.9%; Pred. No. 3.7e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 66
Db 1 GCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 60
QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
Db 61 CAGGGATGGCTATATTTCTGGGAGGCA 87

RESULT 13
US-09-193-853-2
Sequence 2, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-2

Query Match 46.9%; Score 85.4; DB 4; Length 168;
Best Local Similarity 98.9%; Pred. No. 3.7e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 GCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 60
QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
Db 61 CAGGGATGGCTATATTTCTGGGAGGCA 87

RESULT 14
US-09-283-419-3
Sequence 3, Application US/09283419A
Patent No. 6218145
GENERAL INFORMATION:
APPLICANT: Bogosian, Gregg
APPLICANT: O'Neil, Julia P.
APPLICANT: Staub, Jeffrey M.
TITLE OF INVENTION: Bacterial Expression Systems Based on Plastid or
FILE OF INVENTION: Mitochondrial Promoter Combinations
FILE REFERENCE: MOPV040-
CURRENT APPLICATION NUMBER: US/09/283,419A
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: 60/080,432
EARLIER FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 184
TYPE: DNA
ORGANISM: Nicotiana tabacum.
US-09-283-419-3

Query Match 46.9%; Score 85.4; DB 4; Length 184;
Best Local Similarity 98.9%; Pred. No. 3.8e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 66
Db 2 GCTCCCGCGCGTCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 61
QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
Db 62 CAGGGATGGCTATATTTCTGGGAGGCA 88

RESULT 15
US-08-189-256A-24
Sequence 24, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan

;; TITLE OF INVENTION: DNA Constructs and Methods for Stably
;; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
;; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
;; NUMBER OF SEQUENCES: 47
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
;; STREET: 1601 Market Street Suite 720
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-2307
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/189,256A
;; FILING DATE: 31-JAN-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/111,398
;; FILING DATE: 25-AUG-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/518,763
;; FILING DATE: 01-MAY-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Reed, Janet E.
;; REGISTRATION NUMBER: 36,252
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 563-4100
;; TELEFAX: (215) 563-4044
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 258 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-189-256A-24

Query Match 46.9%; Score 85.4; DB 2; Length 258;

Best Local Similarity 98.9%; Pred. No. 4.4e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTCCCGCCGCTGCTTCATGAGATGGTAAGAGGCTCGTGGGATTGACGTGAGGGGG 66
Db 17 GCTCCCGCCGCTGCTTCATGAGATGGTAAGAGGCTCGTGGGATTGACGTGAGGGGG 76
Qy 67 CAGGATGGCTATATTTCTGGAGGA 93
Db 77 CAGGATGGCTATATTTCTGGAGGA 103

Search completed: May 25, 2003, 14:27:51
Job time : 62 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 13:41:49 ; Search time 104 Seconds
(without alignments)

2310.809 Million cell updates/sec

Title: us-09-762-105a-14

Perfect score: 182

Sequence: 1 gagctgcctcccccgcgtc.....tgactggtgacaggtagc 182

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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2	90	49.5	130	9	US-10-109-812-1
3	90	49.5	131	9	US-10-109-812-4
4	84.8	46.6	144	9	US-09-940-925A-163
5	77.8	42.7	202	10	US-09-843-324A-1
6	77.8	42.7	244	10	US-09-843-324A-2
7	70	38.5	89	9	US-10-109-812-41
8	69.2	38.0	399	9	US-10-085-476-12
9	68.8	37.8	97	9	US-09-897-776A-17
10	67.6	37.1	5018	9	US-09-813-718-9
11	66.8	36.7	1057	9	US-09-987-107-51
12	66.8	36.7	1088	9	US-09-987-107-49
13	66.8	36.7	1217	9	US-09-987-107-47
14	66.8	36.7	1219	9	US-09-987-107-53
15	66.8	36.7	1238	9	US-09-987-107-55
16	66.8	36.7	1238	9	US-09-987-107-57
17	66.8	36.7	1238	9	US-09-987-107-59
18	66.8	36.7	1241	9	US-09-987-107-61
19	66.8	36.7	1241	9	US-09-987-107-63

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20 66.8 36.7 1241 9 US-09-987-107-65 Sequence 65, Appl
21 66.8 36.7 1282 9 US-09-987-107-43 Sequence 43, Appl
22 66.8 36.7 1285 9 US-09-987-107-45 Sequence 45, Appl
23 66.8 36.7 1301 9 US-09-987-107-67 Sequence 67, Appl
24 66.8 36.7 4100 9 US-09-813-718-5 Sequence 5, Appl
25 66.4 36.5 4682 9 US-09-813-718-3 Sequence 3, Appl
26 66.4 36.5 4682 9 US-09-813-718-7 Sequence 7, Appl
27 66.4 36.5 5174 9 US-09-813-718-11 Sequence 11, Appl
28 65.6 36.0 4877 9 US-09-976-297-5 Sequence 5, Appl
29 65.4 35.9 656 9 US-09-976-297-7 Sequence 7, Appl
30 65.4 35.9 656 9 US-09-813-718-15 Sequence 15, Appl
31 65.4 35.9 4742 9 US-09-813-718-13 Sequence 13, Appl
32 65.4 35.9 4811 9 US-09-906-209-17 Sequence 17, Appl
33 64.6 35.5 6611 9 US-09-934-900-26 Sequence 26, Appl
34 64.6 35.5 6611 10 US-09-838-718A-7 Sequence 7, Appl
35 62 34.1 5770 10 US-09-838-718A-8 Sequence 8, Appl
36 62 34.1 5870 10 US-09-838-718A-6 Sequence 6, Appl
37 62 34.1 5906 10 US-09-940-235-6 Sequence 6, Appl
38 60.4 33.2 1327 9 US-09-940-235-5 Sequence 5, Appl
39 60.4 33.2 1377 9 US-09-940-235-10 Sequence 10, Appl
40 60.4 33.2 1661 9 US-09-940-235-11 Sequence 11, Appl
41 60.4 33.2 1782 9 US-09-940-235-12 Sequence 12, Appl
42 60.4 33.2 2096 9 US-09-838-718A-5 Sequence 5, Appl
43 59.6 32.7 5230 10 US-09-981-002-5 Sequence 5, Appl
44 59.4 32.6 6714 9 US-10-212-357-1 Sequence 1, Appl
45 58.4 32.1 682 9 US-10-212-357-1 Sequence 1, Appl
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ALIGNMENTS

RESULT 1

US-10-109-812-13

Sequence 13, Application US/10109812

Publication No. US20030088081A1

GENERAL INFORMATION:

APPLICANT: Maligna, Pal

APPLICANT: Lutz, Kerry

TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the

FILE REFERENCE: Rutgers-00-0038 CIP

CURRENT FILING DATE: 2002-03-29

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-06-13

PRIOR FILING DATE: 1999-09-21

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 1049

TYPE: DNA

ORGANISM: tobacco

US-10-109-812-13

Query Match 51.4%; Score 93.6; DB 9; Length 1049;

Best Local Similarity 75.0%; Pred. No. 3.4e-21;

Mismatches 0; Gaps 0;

Matches 11; Conservative 0; Indels 0; Gaps 0;

Query 1 GAGCTCGCTCCCGCCCGCTGTTCAATGAGATGATGAGCGTTCGTTCCACTAGACGTG 60

Sequence 1, Appl

Sequence 4, Appl

Sequence 163, App

Sequence 1, Appl

Sequence 2, Appl

Sequence 41, Appl

Sequence 12, Appl

Sequence 17, Appl

Sequence 9, Appl

Sequence 51, Appl

Sequence 49, Appl

Sequence 47, Appl

Sequence 53, Appl

Sequence 55, Appl

Sequence 57, Appl

Sequence 59, Appl

Sequence 61, Appl

Sequence 63, Appl

Sequence 65, Appl

Sequence 67, Appl

Sequence 69, Appl

Sequence 71, Appl

Sequence 73, Appl

Sequence 75, Appl

Sequence 77, Appl

Sequence 79, Appl

Sequence 81, Appl

Sequence 83, Appl

Sequence 85, Appl

Sequence 87, Appl

Sequence 89, Appl

Sequence 91, Appl

Sequence 93, Appl

Sequence 95, Appl

Sequence 97, Appl

Sequence 99, Appl

Sequence 101, Appl

Sequence 103, Appl

Sequence 105, Appl

Sequence 107, Appl

Sequence 109, Appl

Sequence 111, Appl

Sequence 113, Appl

Sequence 115, Appl

Sequence 117, Appl

Sequence 119, Appl

Sequence 121, Appl

Sequence 123, Appl

Sequence 125, Appl

Sequence 127, Appl

Sequence 129, Appl

Sequence 131, Appl

Sequence 133, Appl

Sequence 135, Appl

Sequence 137, Appl

Sequence 139, Appl

Sequence 141, Appl

Sequence 143, Appl

Sequence 145, Appl

Sequence 147, Appl

Sequence 149, Appl

Sequence 151, Appl

Sequence 153, Appl

Sequence 155, Appl

Sequence 157, Appl

Sequence 159, Appl

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Sequence 163, Appl

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Sequence 175, Appl

Sequence 177, Appl

Sequence 179, Appl

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Sequence 213, Appl

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Sequence 331, Appl

Sequence 333, Appl

Sequence 335, Appl

Sequence 337, Appl

Sequence 339, Appl

Sequence 341, Appl

Sequence 343, Appl

Sequence 345, Appl

Sequence 347, Appl

Sequence 349, Appl

Sequence 351, Appl

Sequence 353, Appl

Sequence 355, Appl

Tue May 27 10:47:40 2003

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 DB 1 GAGCTCGCTCCCGCGCTGTTCAATGAGATGAGAGGCTCGTGGATTGACGTG 60
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 QY 61 AGGGGCGAGGATGCTATATTCTGGGAG 90
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 DB 61 AGGGGCGAGGATGCTATATTCTGGGAG 90
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RESULT 4

US-09-940-925A-163
 ; Sequence 163, Application US/09940925A
 ; Publication No. US2003005438A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BROW, MARY ANN D.
 ; LYAMICHEV, VICTOR I.
 ; OLIVE, DAVID M.
 ; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
 ; PATHOGENS
 ; NUMBER OF SEQUENCES: 165
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MEDLEN & CARROLL
 ; STREET: 220 MONTGOMERY STREET, SUITE 2200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/940,925A
 ; FILING DATE: 10-Jun-2002
 ; CLASSIFICATION: <unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CARROLL, PETER G.
 ; REGISTRATION NUMBER: 32,837
 ; REFERENCE/DOCKET NUMBER: FORS-01756
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 705-8410
 ; TELEFAX: (415) 397-8338
 ; INFORMATION FOR SEQ ID NO: 163:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 144 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Query Match 49.5%; Score 90; DB 9; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.1e-20;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCGCTCCCGCGCTGTTCAATGAGATGAGAGGCTCGTGGATTGACGTG 60
 |||||
 DB 1 GAGCTCGCTCCCGCGCTGTTCAATGAGATGAGAGGCTCGTGGATTGACGTG 60
 |||||
 QY 61 AGGGGCGAGGATGCTATATTCTGGGAG 90
 |||||
 DB 61 AGGGGCGAGGATGCTATATTCTGGGAG 90
 |||||

RESULT 3

US-10-109-812-4
 ; Sequence 4, Application US/10109812
 ; Publication No. US2003008081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliga, Pal
 ; APPLICANT: Cornelle, Sylvie
 ; APPLICANT: Lutz, Kerry
 ; TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the
 ; TITLE OF INVENTION: Plastids of Higher Plants
 ; FILE REFERENCE: Rutgers-00-0038 CIP
 ; CURRENT APPLICATION NUMBER: US/10/109,812
 ; CURRENT FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: PCT/US00/25930
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/211,139
 ; PRIOR FILING DATE: 2000-06-13
 ; PRIOR APPLICATION NUMBER: 60/155,007
 ; PRIOR FILING DATE: 1999-09-21
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 131
 ; TYPE: DNA
 ; ORGANISM: tobacco

Query Match 49.5%; Score 90; DB 9; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2.1e-20;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-843-324A-1
 ; Sequence 1, Application US/09843324A
 ; Patent No. US20020042934A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Staub, Jeffrey
 ; APPLICANT: Ye, Guangning

Query Match 46.5%; Score 84.8; DB 9; Length 144;
 Best Local Similarity 97.7%; Pred. No. 1.2e-18;
 Matches 86; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGGAGACCAACAGGTTTCCCACTAGANATATTTTAACTTTAAGAAGGAGATAT 148
 |||||
 DB 37 AGGGAGACCAACAGGTTTCCCTCTAGANATATTTTAACTTTAAGAAGGAGATAT 96
 |||||
 QY 149 ACATATGGCAAGCATGACTGGTGACAG 176
 |||||
 DB 97 ACATATGGCTAGCATGACTGGTGACAG 124
 |||||

RESULT 5


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; APPLICANT: Broyles, Debra
; TITLE OF INVENTION: Method for the transformation of plant cell plastids
; FILE REFERENCE: 15869/WO
; CURRENT APPLICATION NUMBER: US/09/843,324A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,774
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 202
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-843-324A-1

Query Match      42.7%; Score 77.8; DB 10; Length 202;
Best Local Similarity 97.5%; Pred. No. 3e-16;
Matches 79; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCGCCGTCGTTCAATGAGATGGATAAGAGCGTCGTGGGATTGACGTGAGGGGCGAGGGA 72
   |||||||
Db 11 CCCCCGTCGTTCAATGAGATGGATAAGAGCGTCGTGGGATTGACGTGAGGGGCGAGGGA 70

QY 73 TGGCTATATTTCTGGGAGGGA 93
   |||||||
Db 71 TGGCTATATTTCTGGGAGCGA 91

RESULT 6
US-09-843-324A-2
; Sequence 2, Application US/09843324A
; Patent No. US20020042934A1
; GENERAL INFORMATION:
; APPLICANT: Staub, Jeffrey
; APPLICANT: Ye, Guangning
; APPLICANT: Broyles, Debra
; TITLE OF INVENTION: Method for the transformation of plant cell plastids
; FILE REFERENCE: 15869/WO
; CURRENT APPLICATION NUMBER: US/09/843,324A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,774
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-843-324A-2

Query Match      42.7%; Score 77.8; DB 10; Length 244;
Best Local Similarity 97.5%; Pred. No. 3e-16;
Matches 79; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCGCCGTCGTTCAATGAGATGGATAAGAGCGTCGTGGGATTGACGTGAGGGGCGAGGGA 72
   |||||||
Db 11 CCCCCGTCGTTCAATGAGATGGATAAGAGCGTCGTGGGATTGACGTGAGGGGCGAGGGA 70

QY 73 TGGCTATATTTCTGGGAGGGA 93
   |||||||
Db 71 TGGCTATATTTCTGGGAGCGA 91

RESULT 7
US-10-109-812-41
; Sequence 41, Application US/10109812
; Publication No. US20030088081A1
; GENERAL INFORMATION:
; APPLICANT: Malliga, Pal
```

```
; APPLICANT: Cornelle, Sylvie
; APPLICANT: Lutz, Kerry
; TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the
; FILE REFERENCE: Rutgers-00-0038 CIP
; CURRENT APPLICATION NUMBER: US/10/109,812
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US00/25930
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/211,139
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/155,007
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-109-812-41

Query Match      38.5%; Score 70; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 8.3e-14;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 GAGGAGACCAACACGGTTTCCCACTAGAAATAATTTTGTAACTTTAAGAAGGAGATA 147
   |||||||
Db 19 GAGGAGACCAACACGGTTTCCCACTAGAAATAATTTTGTAACTTTAAGAAGGAGATA 78

QY 148 TACATATGGC 157
   |||||||
Db 79 TACATATGGC 88

RESULT 8
US-10-085-476-12
; Sequence 12, Application US/10085476
; Patent No. US20020164722A1
; GENERAL INFORMATION:
; APPLICANT: De Francesco, Raffaele
; APPLICANT: Tomei, Licia
; APPLICANT: Behrens, Sven-Erik
; TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
; FILE REFERENCE: RNA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL
; FILE REFERENCE: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
; CURRENT APPLICATION NUMBER: US/10/085,476
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 08/952,981
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PCT/IT96/00106
; PRIOR FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: RM95A000343
; PRIOR FILING DATE: 1995-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 399
; TYPE: RNA
; ORGANISM: Rattus norvegicus
US-10-085-476-12

Query Match      38.0%; Score 69.2; DB 9; Length 399;
Best Local Similarity 68.9%; Pred. No. 3.1e-13;
Matches 51; Conservative 20; Mismatches 3; Indels 0; Gaps 0;

QY 90 GGGAGACCAACACGGTTTCCCACTAGAAATAATTTTGTAACTTTAAGAAGGAGATA 149
   |||||||
Db 1 GGGAGACCAACACGGTUUUCCCUAGAAUAUUUUUUUAACUUUAAGAAGGAGAUUA 60

QY 150 CATATGGCAAGCAT 163
   ||:|||||
Db 61 CAUUGGCUAGAAU 74
```

3364 AGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 3423

149 ACATATGGCAAGCA 162
3424 ACATATGCCCAACA 3437

RESULT 11
US-09-987-107-51
; Sequence 51, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE INFORMATION: p7 H6 Ex Cys-Apo A1 plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(882)
; OTHER INFORMATION:
US-09-987-107-51

Query Watch 36.7% Score 66.8; DB 9; Length 1057;
Best Local Similarity 97.1% Pred. No. 3e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

89 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
36 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 95

149 ACATATGGCA 158
96 ACATATGGGA 105

RESULT 12
US-09-987-107-49
; Sequence 49, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 49
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Artificial Sequence

Query Watch 37.1% Score 67.6; DB 9; Length 5018;
Best Local Similarity 94.6% Pred. No. 3.3e-12;
Matches 70; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

89 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148

149 ACATATGGCA 160
77 ACATATGGCATG 88

RESULT 10
US-09-813-718-9
; Sequence 9, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5018
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3428)..(4879)
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: full-length TrpRS in pET20B
US-09-813-718-9

Query Watch 37.1% Score 67.6; DB 9; Length 5018;
Best Local Similarity 94.6% Pred. No. 3.3e-12;
Matches 70; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

89 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148

149 ACATATGGCA 160
77 ACATATGGCATG 88

RESULT 9
US-09-897-776A-17
; Sequence 17, Application US/09897776A
; Publication No. US20030092001A1
; GENERAL INFORMATION:
; APPLICANT: Schnable, Patrick S.
; APPLICANT: Liu, Feng
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING MULTIPLE
; FILE REFERENCE: 08/11-037001
; CURRENT APPLICATION NUMBER: US/09/897,776A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/732,990
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,725
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: TestSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE INFORMATION: Synthetically generated oligonucleotide
US-09-897-776A-17

Query Watch 37.8% Score 68.8; DB 9; Length 97;
Best Local Similarity 97.2% Pred. No. 2.2e-13;
Matches 70; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

89 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
17 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 76

149 ACATATGGCA 160
77 ACATATGGCATG 88

RESULT 9
US-09-897-776A-17
; Sequence 17, Application US/09897776A
; Publication No. US20030092001A1
; GENERAL INFORMATION:
; APPLICANT: Schnable, Patrick S.
; APPLICANT: Liu, Feng
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING MULTIPLE
; FILE REFERENCE: 08/11-037001
; CURRENT APPLICATION NUMBER: US/09/897,776A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/732,990
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,725
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: TestSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE INFORMATION: Synthetically generated oligonucleotide
US-09-897-776A-17

Query Watch 37.8% Score 68.8; DB 9; Length 97;
Best Local Similarity 97.2% Pred. No. 2.2e-13;
Matches 70; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

89 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
17 AGGGAGACCAACAGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 76

149 ACATATGGCA 160
77 ACATATGGCATG 88

```

; FEATURE:
; OTHER INFORMATION: pT/H6 Trip-A-Apo A-1-del 43 - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(918)
; OTHER INFORMATION:
; US-09-987-107-49

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Query Match 36.7%; Score 66.8; DB 9; Length 1088;
Best Local Similarity 97.1%; Pred. NO. 3.1e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGGGAGACCACAACGGTTTCCCACCTAGAAATAATTTTGTAACTTTAGAAAGGAGATAT 148
 Db 36 AGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTAACTTTAGAAAGGAGATAT 95

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RESULT 13
US-09-987-107-47
; Sequence 47, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7 H6 Trip-A-Apo A-1 - A
; NAME/KEY: CDS
; LOCATION: (100)..(1047)
; OTHER INFORMATION:
; US-09-987-107-47

```

Query Match 36.7%; Score 66.8; DB 9; Length 1217;
Best Local Similarity 97.1%; Pred. NO. 3.2e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGGAGACCACAACGGTTCCCACTAGAATAATTTGTCTTAACCTTAAAGAAGGAGATAT 148
|||||
Db 36 AGGAGACCACAACGGTTCCCTCTAGAAAATAATTTGTCTTAACCTTAAAGAAGGAGATAT 95

```

RESULT 14
US-09-987-107-53
; Sequence 53, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107

```

```

: CURRENT FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US 60/264,022
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: DK PA2001 00057
: PRIOR FILING DATE: 2001-01-15
: PRIOR APPLICATION NUMBER: DK PA2000 01682
: PRIOR FILING DATE: 2000-11-10
: NUMBER OF SEQ ID NOS: 91
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 53
: LENGTH: 1217
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: p7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid
: NAME/KEY: CDS
: LOCATION: (100)..(1047)
: OTHER INFORMATION:
: US-09-987-107-53

```

[illegible]

```

1  RESULT 15
2  US-09-987-107-55
3  : Sequence 55, Application US/09987107
4  : Patent No. US20020156007A1
5  : GENERAL INFORMATION:
6  : APPLICANT: GRAVERSEN, Jonas
7  : APPLICANT: MOESTRUP, Soren
8  : TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
9  : FILE REFERENCE: GRAVERSENIA
10 : CURRENT APPLICATION NUMBER: US/09/987,107
11 : CURRENT FILING DATE: 2001-11-13
12 : PRIOR APPLICATION NUMBER: US 60/264,022
13 : PRIOR FILING DATE: 2001-01-26
14 : PRIOR APPLICATION NUMBER: DK PA2001 00057
15 : PRIOR FILING DATE: 2001-01-15
16 : PRIOR APPLICATION NUMBER: DK PA2000 01692
17 : PRIOR FILING DATE: 2000-11-10
18 : NUMBER OF SEQ ID NOS: 91
19 : SOFTWARE: PatentIn version 3.1
20 : SEQ ID NO 55
21 : LENGTH: 1238
22 : TYPE: DNA
23 : NAME: Dna
24 : ORGANISM: Artificial Sequence
25 : FEATURE:
26 : OTHER INFORMATION: pt7H6 Trip-A-Fn-Apo A1 -
27 : NAME/KEY: CDS
28 : LOCATION: (100)..(1068)
29 : OTHER INFORMATION:
30 : US-09-987-107-55

```

	Query Match	36.7%	Score 66.8;	DB 9;	Length 1238;
	Best Local Similarity	97.1%;	Pred. No. 3,2e-13;		
	Matches 68;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	89	AGGGAGACCACAAAGGTTTCCCACTAGAAAATAATTTCTTTTAACCTTTAAGAAGGAGATAT	148		
Dd	36	AGGGAGACCACAAAGGTTTCCCTCTAGAAAATAATTTCTTTTAACCTTTAAGAAGGAGATAT	95		
Qy	149	ACATATGGCA	158		

us-09-762-105a-14.rnpb

Tue May 27 10:47:40 2003

Db 96 ACATATGGGA 105

Search completed: May 25, 2003, 14:29:51
Job time : 107 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 13:23:39 ; Search time 1416 Seconds
(without alignments)
2081.623 Million cell updates/sec

Title: US-09-762-105a-14
Perfect score: 182
Sequence: 1 gagctcgtccccccgctc.....tgactggaggacagctagc 182

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.6	39.9	787	17	BH558942
2	72.4	39.8	775	17	BH424823
3	72.2	39.7	735	17	BH509684
4	72.2	39.7	838	17	BH472349
5	71.8	39.5	770	17	BH668002
6	71.8	39.5	836	17	BH709230

7	71.8	39.5	841	17	BH653765
8	71.6	39.3	724	17	BH418480
9	71	39.0	805	17	BH474481
10	71	39.0	847	17	BH721450
11	70.8	38.9	169	17	AQ962940
12	70.8	38.9	199	17	BH537952
13	70.8	38.9	238	17	BH537952
14	70.8	38.9	292	17	BH474703
15	70.8	38.9	305	17	BH646726
16	70.8	38.9	322	17	BH705426
17	70.8	38.9	367	17	BH430502
18	70.8	38.9	368	17	BH493122
19	70.8	38.9	416	17	BH664090
20	70.8	38.9	419	17	BH662193
21	70.8	38.9	422	17	BH475597
22	70.8	38.9	423	17	BH653681
23	70.8	38.9	434	17	BH545732
24	70.8	38.9	434	17	BH678091
25	70.8	38.9	441	17	BH657205
26	70.8	38.9	448	17	BH689289
27	70.8	38.9	450	17	BH725279
28	70.8	38.9	451	17	BH719345
29	70.8	38.9	459	17	BH562132
30	70.8	38.9	466	17	BH541747
31	70.8	38.9	488	17	BH740372
32	70.8	38.9	489	17	BH718684
33	70.8	38.9	475	17	BH669610
34	70.8	38.9	475	17	BH700638
35	70.8	38.9	482	17	BH649351
36	70.8	38.9	484	17	BH650341
37	70.8	38.9	487	17	BH734521
38	70.8	38.9	488	17	BH648975
39	70.8	38.9	497	17	AQ967359
40	70.8	38.9	501	17	BH717042
41	70.8	38.9	503	17	BH654995
42	70.8	38.9	506	17	BH694130
43	70.8	38.9	507	17	BH491584
44	70.8	38.9	508	17	BH675079
45	70.8	38.9	511	17	BH717427

ALIGNMENTS

RESULT 1
BH558942
LOCUS BOHL272TR BOHL Brassica oleracea genomic clone BOHL272, DNA
DEFINITION 787 bp
ACCESSION BH558942
VERSION BH558942.1 GI:17810722
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 787)
TOWN,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
AUTHORS Whole genome shotgun sequencing of Brassica oleracea
TITLE Unpublished (2001)
JOURNAL
COMMENT Other_GSSs: BOHL272TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends,
Location/Qualifiers
source
1. 787

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/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHL272"
/clone_lib="BOHL"
/notes="Vector: pHS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHS1 using BstXI linkers"
BASE COUNT 215 a 139 c 184 g 249 t
ORIGIN
Query Match 39.9%; Score 72.6; DB 17; Length 787;
Best Local Similarity 85.3%; Pred. No. 2.1e-12;
Matches 81; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 4 CTGCTCCCCCGCTGTCATGAGTGAATGATGAGAGGCTCGTGGGATTGACGTGAGG 63
Db 664 CTGCTCCCCCGCTGTCATGAGTGAATGATGAGAGGCTCGTGGGATTGACGTGAGG 723
QY 64 GGGCAGGATGCTATATTTCTGGGAGGACCA 98
Db 724 GGGTAGGGTAGCTATATTTCTGGGAGGACTCCA 758

RESULT 2
BH424823 775 bp DNA linear GSS 12-DEC-2001
LOCUS BOHNJ79TR BOHN Brassica oleracea genomic clone BOHNJ79, DNA
DEFINITION
ACCESSION BH424823.1 GI:17610551
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 775)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOHNJ79TR
Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..775
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHL272"
/clone_lib="BOHL"
/notes="Vector: pHS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHS1 using BstXI linkers"
BASE COUNT 203 a 161 c 247 g 164 t
ORIGIN
Query Match 39.8%; Score 72.4; DB 17; Length 775;
Best Local Similarity 87.8%; Pred. No. 2.5e-12;
Matches 79; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 4 CTGCTCCCCCGCTGTCATGAGTGAATGATGAGAGGCTCGTGGGATTGACGTGAGG 63
Db 8 CTGCTCCCCCGCTGTCATGAGTGAATGATGAGAGGCTCGTGGGATTGACGTGAGG 67
QY 64 GGGCAGGATGCTATATTTCTGGGAGGCA 93
Db 68 GGGTAGGGTAGCTATATTTCTGGGAGGCA 97

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RESULT 3
BH509684 735 bp DNA linear GSS 13-DEC-2001
LOCUS BOHSH07TF BOHS Brassica oleracea genomic clone BOHSH07, DNA
DEFINITION
ACCESSION BH509684
VERSION BH509684.1 GI:17717774
KEYWORDS
SOURCE
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 735)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOHSH07TR
Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..735
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHSH07"
/clone_lib="BOHS"
/notes="Vector: pHS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHS1 using BstXI linkers"
BASE COUNT 205 a 133 c 172 g
ORIGIN
Query Match 39.7%; Score 72.2; DB 17; Length 735;
Best Local Similarity 86.0%; Pred. No. 2.8e-12;
Matches 80; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 4 CTGCTCCCCCGCTGTCATGAGTGAATGATGAGAGGCTCGTGGGATTGACGTGAGG 63
Db 521 CTGCTCCCCCGCTGTCATGAGTGAATGATGAGAGGCTCGTGGGATTGACGTGAGG 580
QY 64 GGGCAGGATGCTATATTTCTGGGAGGAGAC 96
Db 581 GGGTAGGGTAGCTATATTTCTGGGAGGAGAC 613

RESULT 4
BH472349 838 bp DNA linear GSS 13-DEC-2001
LOCUS BOGIY45TF BOGI Brassica oleracea genomic clone BOGIY45, DNA
DEFINITION
ACCESSION BH472349
VERSION BH472349.1 GI:17680460
KEYWORDS
SOURCE
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 838)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOGIY45TR
Contact: Chris Town

```

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtonnet@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES

source

Location/Qualifiers

1. .838
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BOGI45"
/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 233 a 142 c 191 g 272 t

ORIGIN

Query Match 39.7%; Score 72.2; DB 17; Length 838;
Best Local Similarity 86.0%; Pred. No. 2.9e-12;
Matches 80; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 CTCGCTCCCGCGCTCAATGAGTAAGAGGCTCGTGGATTGACGTGAGG 63
DB 720 CTTGCTCCCTCGCTGATCGAATAAGATGAGGCTCGTGGATTGACGTGAGG 779
QY 64 GGCAGGAGGTGCTATATTTCTGGGAGGAGAC 96
DB 780 GGGTAGGGGTAGCTATATTTCTGGGAGGAAAC 812

RESULT 5

BH668002

LOCUS

DEFINITION BOMLN95TF BO_2_3_KB Brassica oleracea genomic clone BOMLN95, DNA

ACCESSION

BH668002

VERSION

BH668002.1

KEYWORDS

GSS.

SOURCE

Brassica oleracea.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 770)

AUTHORS

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.

TITLE

Whole genome shotgun sequencing of Brassica oleracea

JOURNAL

Unpublished (2001)

COMMENT

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtonnet@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

1. .770

/organism="Brassica oleracea"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOMLN95"

/clone_lib="BO_2_3_KB"

/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 204 a 162 c 246 g 158 t

ORIGIN

Query Match 39.5%; Score 71.8; DB 17; Length 770;
Best Local Similarity 86.8%; Pred. No. 3.8e-12;

Matches 79; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 3 GCTGCTCCCGCGCTCAATGAGTAAGAGGCTCGTGGATTGACGTGAG 62
DB 1 GCITGCTCCCTCGCTGATCGAATAAGATGAGGCTCGTGGATTGACGTGAG 60
QY 63 GGGCAGGAGGTGCTATATTTCTGGGAGGGA 93
DB 61 GGGTAGGGGTAGCTATATTTCTGGGAGCGA 91

RESULT 6

BH709230

LOCUS

DEFINITION BOMNO33TR BO_2_3_KB Brassica oleracea genomic clone BOMNO33, DNA

ACCESSION

BH709230

VERSION

BH709230.1

KEYWORDS

GSS.

SOURCE

Brassica oleracea.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 836)

AUTHORS

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.

TITLE

Whole genome shotgun sequencing of Brassica oleracea

JOURNAL

Unpublished (2001)

COMMENT

Other_GSSs: BOMNO33TF

Contact: Chris Town

TIGR

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Fax: 301-838-0208

Email: cdtonnet@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1. .836

/organism="Brassica oleracea"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOMNO33"

/clone_lib="BO_2_3_KB"

/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 233 a 146 c 195 g 262 t

ORIGIN

Query Match 39.5%; Score 71.8; DB 17; Length 836;
Best Local Similarity 68.0%; Pred. No. 3.9e-12;
Matches 100; Conservative 0; Mismatches 47; Indels 0; Gaps 0;QY 4 CTCGCTCCCGCGCTCAATGAGTAAGAGGCTCGTGGATTGACGTGAGG 63
DB 664 CTTGCTCCCTCGCTGATCGAATAAGATGAGGCTCGTGGATTGACGTGAGG 723
QY 64 GGCAGGAGGTGCTATATTTCTGGGAGGAGCACCACACACGGTTCCCACTAGAAATATT 123
DB 724 GGGTAGGGGTAGCTATATTTCTGGGAGGAACTCGGAATATGAAGCGCATGATACC 783
QY 124 TTGTTTAACCTTTAAGAAGGAGATATAC 150
DB 784 AAGTATGACTTGGAAATGAAGAAATTC 810

RESULT 7

BH653765

LOCUS

DEFINITION BOMNX13TF BO_2_3_KB Brassica oleracea genomic clone BOMNX13, DNA

ACCESSION

BH653765

Tue May 27 10:47:42 2003

```

VERSION      BH653765.1  GI:18711917
KEYWORDS     GSS.
SOURCE       Brassica oleracea.
ORGANISM     Brassica oleracea.
REFERENCE    1. (bases 1 to 841)
AUTHORS      Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE        Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA.
              Tel: 301-838-3523
              Fax: 301-838-0208
              Email: cdtownetigr.org
              DNA is from a doubled haploid provided by Tom Osborn.
              Seq primer: TF
              Class: sheared ends.
              Location/Qualifiers
                1. .841
                  /organism="Brassica oleracea"
                  /strain="TO1000DH3"
                  /db_xref="taxon:3712"
                  /clone_lib="BO_2_3_KB"
                  /note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
                  genomic DNA inserted into PHOS1 using BstXI linkers."
              BASE COUNT      236 a 146 c 194 g 265 t
              ORIGIN
                1. .841
                  39.5%; Score 71.8; DB 17; Length 841;
                  Best Local Similarity 68.0%; Pred. No. 3.9e-12;
                  Matches 100; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
                  QY 4 CTCGCTCCCGCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 63
                  Db 675 CTTCCTCCCTCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 734
                  QY 64 GGGCAGGAGGATGCTATATTTCTGGGAGGAGCACCACGCTTTCCCACTAGAAATAATT 123
                  Db 735 GGGTAGGGTGTGCTATATTTCTGGGAGGAGCATTCTATGCGAATATGAAGCGCATGGATACA 794
                  QY 124 TTGTTTAACCTTTAAGAAGGAGATATAC 150
                  Db 795 AAGTAGTACTTGGAAATGAAGACATTC 821

              RESULT 8
              BH418480/c
              LOCUS      BH418480      724 bp      DNA      linear      GSS 12-DEC-2001
              DEFINITION  BOGX95TR BOGX Brassica oleracea genomic clone BOGX95, DNA
              sequence.
              ACCESSION  BH418480
              VERSION     BH418480.1  GI:17604208
              KEYWORDS    GSS.
              SOURCE      Brassica oleracea.
              ORGANISM     Brassica oleracea.
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
              1 (bases 1 to 724)
              Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
              Whole genome shotgun sequencing of Brassica oleracea
              Unpublished (2001)
              Other_GSSs: BOGX95TF
              Contact: Chris Town
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA.
              Tel: 301-838-3523
              Fax: 301-838-0208
              Email: cdtownetigr.org

              Query Match      39.5%; Score 71.8; DB 17; Length 841;
              Best Local Similarity 68.0%; Pred. No. 3.9e-12;
              Matches 100; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
              QY 4 CTCGCTCCCGCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 63
              Db 675 CTTCCTCCCTCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 734
              QY 64 GGGCAGGAGGATGCTATATTTCTGGGAGGAGCACCACGCTTTCCCACTAGAAATAATT 123
              Db 735 GGGTAGGGTGTGCTATATTTCTGGGAGGAGCATTCTATGCGAATATGAAGCGCATGGATACA 794
              QY 124 TTGTTTAACCTTTAAGAAGGAGATATAC 150
              Db 795 AAGTAGTACTTGGAAATGAAGACATTC 821

              DNA is from a doubled haploid provided by Tom Osborn.
              Seq primer: TF
              Class: sheared ends.
              Location/Qualifiers
                1. .805
                  /organism="Brassica oleracea"
                  /strain="TO1000DH3"
                  /db_xref="taxon:3712"
                  /clone_lib="BOHY09"
                  /note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
                  genomic DNA inserted into PHOS1 using BstXI linkers."
              BASE COUNT      221 a 139 c 182 g 263 t
              ORIGIN
                1. .805
                  39.0%; Score 71.1; DB 17; Length 805;
                  Best Local Similarity 84.2%; Pred. No. 7e-12;
                  Matches 80; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
                  QY 4 CTCGCTCCCGCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 63
                  Db 707 CTTCCTCCCTCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 648
                  QY 64 GGGCAGGAGGATGCTATATTTCTGGGAGGAGCACC 97
                  Db 647 GGGTAGGGTGTGCTATATTTCTGGGAGGAGCCTCC 614

              RESULT 9
              BH474481
              LOCUS      BH474481      805 bp      DNA      linear      GSS 13-DEC-2001
              DEFINITION  BOHY09TR BOHY Brassica oleracea genomic clone BOHY09, DNA
              sequence.
              ACCESSION  BH474481
              VERSION     BH474481.1  GI:17682592
              KEYWORDS    GSS.
              SOURCE      Brassica oleracea.
              ORGANISM     Brassica oleracea.
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
              1 (bases 1 to 805)
              Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
              Whole genome shotgun sequencing of Brassica oleracea
              Unpublished (2001)
              Other_GSSs: BOHY09TF
              Contact: Chris Town
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA.
              Tel: 301-838-3523
              Fax: 301-838-0208
              Email: cdtownetigr.org
              DNA is from a doubled haploid provided by Tom Osborn.
              Seq primer: TF
              Class: sheared ends.
              Location/Qualifiers
                1. .805
                  /organism="Brassica oleracea"
                  /strain="TO1000DH3"
                  /db_xref="taxon:3712"
                  /clone_lib="BOHY09"
                  /note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
                  genomic DNA inserted into PHOS1 using BstXI linkers."
              BASE COUNT      221 a 139 c 182 g 263 t
              ORIGIN
                1. .805
                  39.0%; Score 71.1; DB 17; Length 805;
                  Best Local Similarity 84.2%; Pred. No. 7e-12;
                  Matches 80; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
                  QY 4 CTCGCTCCCGCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 63
                  Db 707 CTTCCTCCCTCGCTCGTCAATGAGATGAGTAAAGAGGCTCGTGGGATTCAGCTGAGG 648
                  QY 64 GGGCAGGAGGATGCTATATTTCTGGGAGGAGCACC 97
                  Db 647 GGGTAGGGTGTGCTATATTTCTGGGAGGAGCCTCC 614

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[illegible]

PR	29-APR-1999;	99US-0131611.
PR	11-JUN-1999;	99US-0138764.
PA	(RUTF) UNIV RUTGERS STATE NEW JERSEY.	
PI	Malliga P, Kuroda H, Khan MS;	
PI	WPI: 2000-205525/18.	
DR	New recombinant DNA constructs, for expressing high levels of	
PT	heterologous protein in plastids of higher plants, includes promoter, a	
PT	leader sequence and a downstream box element -	
XX	Claim 4; Fig 3D; 164pp; English.	
XX	The present sequence represents a chimeric plasmid RNA operon	
CC	omega-type (Prn) promoter with the T7 phage gene and plastid	
CC	downstream box. The chimeric promoter is used, as a 5' regulatory	
CC	sequence, to produce recombinant DNA constructs for expressing	
CC	heterologous proteins in the plastids of higher plants. The DNA	
CC	constructs comprise a 5' regulatory region which includes a promoter	
CC	element, a leader sequence and a downstream box element operably linked	
CC	to a coding region of the heterologous protein. The chimeric regulatory	
CC	region enhances translational efficiency of an mRNA molecule encoded by	
CC	the DNA construct. The DNA constructs are used for producing transformed	
CC	monocot and dicot plants having high levels of heterologous protein	
CC	expression. They can be used to drive expression of proteins with	
CC	agronomic, industrial or pharmaceutical importance, including production	
CC	of vaccines, healthcare products like human haemoglobin, industrial or	
CC	household enzymes. Plants which can be transformed with the constructs	
CC	of the invention include maize, millet, sorghum, sugar cane, rice,	
CC	wheat, barley, oat, rye or turf grass.	
XX	Sequence 182 BP; 49 A; 34 C; 56 G; 43 T; 0 other;	
SQ		
Query Match	100.0%; Score 182; DB 21; Length 182;	
Best Local Similarity	100.0%; Pred. No. 1.2e-50;	
Matches 182; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 GAGCTCGCTCCCCGGTGTTCATGAATGAGATTAAGAGGCTCGTGAGATTGACGTG 60	
Db		
Oy	1 GAGCTCGCTCCCCGGTGTTCATGAATGAGATTAAGAGGCTCGTGAGATTGACGTG 60	
Db		
Oy	61 AGGGGCCAGGATGGCTATATTTCTGGAGGGAGACCACCAACGGTTTTCCCACCTAGAATA 120	
Db		
Oy	121 ATTTTGTAACTTTAAGAGGAGATATACATATGGCAAGCATGACTGGTGGACAGGCTA 180	
Db		
Oy	121 ATTTTGTAACTTTAAGAGGAGATATACATATGGCAAGCATGACTGGTGGACAGGCTA 180	
Db		
Oy	181 GC 182	
Db	181 GC 182	
RESULT 2		
ID	AZ61384 standard; DNA; 1961 BP.	
XX	AZ61384;	
AC		
XX	19-JUN-2000 (first entry)	
DE	Nucleotide sequence of DNA construct FLARE11-S3.	
XX	Green fluorescent protein; GFP; aadA; protein expression; vaccine;	
KW	haemoglobin; enzyme; psbA; T7 phage gene 10; ss.	
OS	Synthetic.	
OS	Unidentified.	
OS	Aequorea victoria.	
XX		

CC The present sequence represents a chimeric plastid rRNA operon
 CC omega-type (Prn) promoter with the T7 phage gene and Escherichia coli
 CC downstream box. The chimeric promoter is used, as a 5' regulatory
 CC sequence, to produce recombinant DNA constructs for expressing
 CC heterologous proteins in the plastids of higher plants. The DNA
 CC constructs comprise a 5' regulatory region which includes a promoter
 CC element, a leader sequence and a downstream box element operably linked
 CC to a coding region of the heterologous protein. The chimeric regulatory
 CC region enhances translational efficiency of an mRNA molecule encoded by
 CC the DNA construct. The DNA constructs are used for producing transformed
 CC monocot and dicot plants having high levels of heterologous protein
 CC expression. They can be used to drive expression of proteins with
 CC agronomic, industrial or pharmaceutical importance, including production
 CC of vaccines, healthcare products like human haemoglobin, industrial or
 CC household enzymes. Plants which can be transformed with the constructs
 CC of the invention include maize, millet, sorghum, sugar cane, rice,
 CC wheat, barley, oat, rye or turf grass.

XX Sequence 182 BP; 47 A; 38 C; 52 G; 45 T; 0 other;

Query Match 90.38; Score 164.4; DB 21; Length 182;
 Best Local Similarity 94.08; Pred. No. 8.3e-45;
 Matches 171; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCTCGCTCCCGCCGCTTCAATGAGATGAGTGAAGAGGCTCGTGGATTGACGTG 60
 Db 1 GAGCTCGCTCCCGCCGCTTCAATGAGATGAGTGAAGAGGCTCGTGGATTGACGTG 60
 QY 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACAGGTTTCCCACTAGAAATA 120
 Db 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACAGGTTTCCCACTAGAAATA 120
 QY 121 ATTTGTTTAACTTTAAGAGGAGATATACATATGGAAGCATGACTGGTGACAGGCTA 180
 Db 121 ATTTGTTTAACTTTAAGAGGAGATATACATATGGAAGCATGACTGGTGACAGGCTA 180
 QY 181 GC 182
 Db 181 GC 182

RESULT 5
 AAZ61375

ID AAZ61375 standard; DNA; 161 BP.

XX AAZ61375;

XX 19-JUN-2000 (first entry)

XX Nucleotide sequence of chimeric promoter PrnLT7g10-DB.

XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
 XX Prn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT promoter 7..89

FT /*tag= a

FT /note= "Prn plastid promoter"

FT misc_signal 141..144

FT /*tag= b

FT /note= "Shine-Dalgarno sequence"

XX WO200007431-A1.

XX 17-FEB-2000.

XX 03-AUG-1999; 99WO-US17806.

XX 03-AUG-1998; 98US-0095163.

XX 03-AUG-1998; 98US-0095167.

XX 15-DEC-1998; 98US-0112257.

PR 29-APR-1999; 99US-0131611.
 PR 11-JUN-1999; 99US-0138764.
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Maliga P, Kuroda H, Khan MS;

XX WPI; 2000-205525/18.

XX New recombinant DNA constructs, for expressing high levels of
 PT heterologous protein in plastids of higher plants, includes promoter, a
 PT leader sequence and a downstream box element.

XX Claim 4: Fig 3D; 164pp; English.

XX The present sequence represents a chimeric plastid rRNA operon
 CC omega-type (Prn) promoter with the T7 phage gene and a synthetic
 CC downstream box. The chimeric promoter is used, as a 5' regulatory
 CC sequence, to produce recombinant DNA constructs for expressing
 CC heterologous proteins in the plastids of higher plants. The DNA
 CC constructs comprise a 5' regulatory region which includes a promoter
 CC element, a leader sequence and a downstream box element operably linked
 CC to a coding region of the heterologous protein. The chimeric regulatory
 CC region enhances translational efficiency of an mRNA molecule encoded by
 CC the DNA construct. The DNA constructs are used for producing transformed
 CC monocot and dicot plants having high levels of heterologous protein
 CC expression. They can be used to drive expression of proteins with
 CC agronomic, industrial or pharmaceutical importance, including production
 CC of vaccines, healthcare products like human haemoglobin, industrial or
 CC household enzymes. Plants which can be transformed with the constructs
 CC of the invention include maize, millet, sorghum, sugar cane, rice,
 CC wheat, barley, oat, rye or turf grass.

XX Sequence 161 BP; 43 A; 30 C; 48 G; 40 T; 0 other;

Query Match 87.68; Score 159.4; DB 21; Length 161;
 Best Local Similarity 99.48; Pred. No. 3.6e-43;

Matches 160; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCTCGCTCCCGCCGCTTCAATGAGATGAGTGAAGAGGCTCGTGGATTGACGTG 60

Db 1 GAGCTCGCTCCCGCCGCTTCAATGAGATGAGTGAAGAGGCTCGTGGATTGACGTG 60

QY 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACAGGTTTCCCACTAGAAATA 120

Db 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACAGGTTTCCCACTAGAAATA 120

QY 121 ATTTTGTGTTAACTTTAAGAGGAGATATACATATGGAAGCATGACTGGTGACAGGCTA 161

Db 121 ATTTTGTGTTAACTTTAAGAGGAGATATACATATGGAAGCATGACTGGTGACAGGCTA 161

RESULT 6

AAZ88175

ID AAZ88175 standard; DNA; 168 BP.

XX AAZ88175;

XX 25-APR-2000 (first entry)

XX Prn/G10L fusion nucleic acid sequence.

XX Tobacco; ribosome binding site; aprotinin; herbicide tolerance; plastid;

XX human growth hormone; insulin; ds.

XX Nicotiana sp.

XX Synthetic.

XX WO200003022-A2.

XX 20-JAN-2000.

XX 10-JUL-1999; 99WO-US15472.

Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 GAGTCTGCTCCCGCGCTGTTCAATGAGATGAGTAAGAGGCTCTGGGATTGACGTG 60
|||||
Db 1 GAGTCTGCTCCCGCGCTGTTCAATGAGATGAGTAAGAGGCTCTGGGATTGACGTG 60
|||||

Qy 61 AGGGGCGAGGATGCTATATTTCTGGGAGGAGACCAACACGTTTCCCACTAGAAATA 120
|||||
Db 61 AGGGGCGAGGATGCTATATTTCTGGGAGGAGTAATTAACGATCGACGTGCAAGCGGACATT 120
|||||

Qy 121 ATTTTGTAACTTTAAGAGGAGATACATATG 156
|||||
Db 121 TATTTAAATCGATAATTTTTCGAAAACATTTTCG 156
|||||

RESULT 14
AAZ61369
ID AAZ61369 standard; DNA; 153 BP.
AC AAZ61369;
XX
DT
DT 19-JUN-2000 (first entry)
XX
XX Nucleotide sequence of chimeric promoter Prn1psbB-DB.
DE
XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
KW Prn promoter; psbB; protein expression; vaccine; enzyme; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Promoter 7..89
FT /*tag= a
FT /note= "Prn plastid promoter"
FT misc_signal 138..142
FT /*tag= b
FT /note= "Shine-Dalgarno sequence"
XX
XX WO200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Kuroda H, Khan MS;
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
PT heterologous protein in plastids of higher plants, includes promoter, a
PT leader sequence and a downstream box element -
XX
XX Claim 3; Fig 3B; 164pp; English.
XX
XX The present sequence represents a chimeric plastid rRNA operon
CC omega-type (Prn) promoter with psbB translation control sequences,
CC without a downstream box. The chimeric promoter is used, as a 5',
CC regulatory sequence, to produce recombinant DNA constructs for expressing
CC heterologous proteins in the plastids of higher plants. The DNA
CC constructs comprise a 5' regulatory region which includes a promoter
CC element, a leader sequence and a downstream box element operably linked
CC to a coding region of the heterologous protein. The chimeric regulatory
CC region enhances translational efficiency of an mRNA molecule encoded by
CC the DNA construct. The DNA constructs are used for producing transformed
CC monocot and dicot plants having high levels of heterologous protein

CC expression. They can be used to drive expression of proteins with
CC agronomic, industrial or pharmaceutical importance, including production
CC of vaccines, healthcare products like human haemoglobin, industrial or
CC household enzymes. Plants which can be transformed with the constructs
CC of the invention include maize, millet, sorghum, sugar cane, rice,
CC wheat, barley, oat, rye or turf grass.
XX
SQ Sequence 153 BP; 36 A; 27 C; 47 G; 43 T; 0 other;
Query Match 50.7%; Score 92.2; DB 21; Length 153;
Best Local Similarity 92.4%; Pred. No. 7.6e-21;
Matches 97; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GAGTCTGCTCCCGCGCTGTTCAATGAGATGAGTAAGAGGCTCTGGGATTGACGTG 60
|||||
Db 1 GAGTCTGCTCCCGCGCTGTTCAATGAGATGAGTAAGAGGCTCTGGGATTGACGTG 60
|||||

Qy 61 AGGGGCGAGGATGCTATATTTCTGGGAGGAGACCAACACGTT 105
|||||
Db 61 AGGGGCGAGGATGCTATATTTCTGGGAGGCAATGCAATAAAGTT 105
|||||

RESULT 15
AAZ61372
ID AAZ61372 standard; DNA; 185 BP.
XX
AC AAZ61372;
XX
DT 19-JUN-2000 (first entry)
XX
XX Nucleotide sequence of chimeric promoter Prn1psbA-DB(+GC).
DE
XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
KW Prn promoter; psbA; protein expression; vaccine; enzyme; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Promoter 7..89
FT /*tag= a
FT /note= "Prn plastid promoter"
FT misc_signal 141..144
FT /*tag= b
FT /note= "Shine-Dalgarno sequence"
XX
XX WO200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTE) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Kuroda H, Khan MS;
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
PT heterologous protein in plastids of higher plants, includes promoter, a
PT leader sequence and a downstream box element -
XX
XX Claim 3; Fig 3C; 164pp; English.
XX
XX The present sequence represents a chimeric plastid rRNA operon
CC omega-type (Prn) promoter with psbA translation control sequences,
CC without a downstream box. The chimeric promoter is used, as a 5',
CC regulatory sequence, to produce recombinant DNA constructs for expressing
CC heterologous proteins in the plastids of higher plants. The DNA
CC constructs comprise a 5' regulatory region which includes a promoter
CC element, a leader sequence and a downstream box element operably linked
CC to a coding region of the heterologous protein. The chimeric regulatory
CC region enhances translational efficiency of an mRNA molecule encoded by
CC the DNA construct. The DNA constructs are used for producing transformed
CC monocot and dicot plants having high levels of heterologous protein

heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter element, a leader sequence and a downstream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing transformed monocot and dicot plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.

Sequence 185 BP; 47 A; 35 C; 51 G; 52 T; 0 other;

Query Match 50.7%; Score 92.2; DB 21; Length 185;
Best Local Similarity 88.5%; Pred. NO. 8.2e-21;
Matches 100; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GAGCTCGCTCCCCCGCGTCTGTTCAATGACAATGGATTAAGAGGCTCGTGGGATTGACCTG 60

Db 1 GAGCTCGCTCCCCCGCGTTCATGAGAAATGAGAGGCTCGTGGGATTGACGTG 60

Qy 61 AGGGGCGAGGGATGGCTATATTCTGGAGGGAGACCACACACGGTTTCCCACT 113

Db 61 AGGGGGCAGCGATGGCTATATTTCTGGGAGCAAAAAGCCCTTCCATGTTCTATT 113

Search completed: May 25, 2003, 13:45:18
Job time : 213 secs